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CM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 01:54:35 ; Search time 8415.96 seconds

(without alignments)
11057.263 Million cell updates/sec

Title: US-09-508-377-10_COPY_1058_3204

Perfect score: 2147
Sequence: 1 cgcagcttcaccccccgc.....tcgacatactatgaccagag 2147

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb ba:*
2: gb hcg:*
3: gb in:*
4: gb om:*
5: gb ov:*
6: gb pa:*
7: gb pl:*
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15: em ba:*
16: em fun:*
17: em hum:*
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24: em ph:*
25: em pl:*
26: em ro:*
27: em stg:*
28: em un:*
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31: em hcg_hum:*
32: em hcg_hum:*
33: em hcg_mus:*
34: em hcg_mus:*
35: em hcg_mus:*
36: em hcg_mus:*
37: em hcg_vrt:*
38: em sv:*
39: em hcgo_hum:*
40: em hcgo_hum:*
41: em hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2147	100.0	11463	6 AX031271	AX031271 Sequence
2	2124	98.9	11475	8 AF38431	AF38431 Aegilops
3	1197	55.8	1852	8 AF064562	AF064562 Hordeum v
4	243	11.3	2853	8 AR340173	AR340173 Sequence
5	243	11.3	2853	8 TA066376	TA066376 Triticum ae
6	238.2	11.1	2549	8 BT008928	BT008928 Triticum
7	235	10.9	2726	8 AF38432	AF38432 Triticum
8	235	10.9	2970	8 TASBA2	TASBA2 Triticum
9	233.4	10.9	2970	8 AF286319	AF286319 Triticum
10	201.4	9.4	2554	8 AF064560	AF064560 Hordeum v
11	149	6.9	3094	8 AY357072	AY357072 Triticum
12	139.8	6.5	159683	2 OSUN00286	OSUN00286
13	135.8	6.3	2364	6 E14723	E14723
14	135.8	6.3	3015	6 E14723	E14723
15	135.8	6.3	3015	8 AB023498	AB023498 Oryza sat
16	117.8	5.5	2655	6 AX654742	AX654742 Sequence
17	116	5.4	2304	6 AX755783	AX755783 Sequence
18	90.8	4.2	2446	6 AR427891	AR427891 Sequence
19	90.8	4.2	2780	8 AF064561	AF064561 Hordeum v
20	90.8	4.2	2795	8 ZMU65948	ZMU65948 Zea mays st
21	89.8	4.2	3960	8 AF064563	AF064563 Hordeum v
22	81.4	3.8	151703	8 AP004790	AP004790 Oryza sat
23	80.2	3.7	4668	8 AF28486	AF28486 Zea mays
24	79.4	3.7	2918	6 E08183	E08183 Gene of sca
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26	78.6	3.7	2307	6 AX755372	AX755372 Sequence
27	73.8	3.4	23449	8 AF072725	AF072725 Zea mays
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ALIGNMENTS

RESULT 1
AX031271
LOCUS AX031271 11463 bp DNA
DEFINITION Sequence 10 from Patent WO9914314.
ACCESSION AX031271
VERSION AX031271.1 GI:10278603
KEYWORDS
SOURCE Aegilops tauschii
ORGANISM Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Aegilops.
REFERENCE 1
AUTHORS Li Z., Morell M. and Rahman, S.
TITLE Regulation of gene expression in plants

JOURNAL Patent: WO 9914314-A 10 25-MAR-1999;
GOODMAN FIELDER LTD (AU) ; LI ZHONGYI (AU) ; MORELL MATTHEW (AU) ;
RAHMAN SADEOUR (AU) ; UNIV AUSTRALIAN (AU) ; COMM SCI ENT IND RES
ORG (AU) ; GROUPE LIMAGRAIN PACIFIC PTY L (AU)

FEATURES
Source Location/Qualifiers
1. 11463
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/mol_type="unassigned DNA"
/db_xref="taxon:37682"
/tissue_type="ENDOSPERM"

misc_feature
1. 11463
/product="COMPLETE SEQUENCE OF THE STARCH BRANCHING ENZYME
II GENE"

ORIGIN

Query Match 100.0%; Score 2147; DB 6; Length 11463;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGCAGGCTTCACCCCGCCGACACGTTGCTCCCTTCATCGCTTCATTAATA 60
1058 CGCAGGCTTCACCCCGCCGACACGTTGCTCCCTTCATCGCTTCATTAATA 1117

QY 61 TCTTCATCACTCGGAGTTCCGCGCTGCATTTGGCCGCGGTTGAGTAGATCGGCGA 120
DB 1118 TCTTCATCACTCGGAGTTCCGCGCTGCATTTGGCCGCGGTTGAGTAGATCGGCGA 1177

QY 121 CTGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 180
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QY 181 GTGTGCG 240
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QY 361 GCTGTCCCAATGATCTCCATGATGAGAGATGATGATGATGATGATGATGATGAT 420
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QY 421 CTGAACCTGATATTTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
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QY 541 CTGTTCTTGTGATCACTGCAAGTTGGCGTTTTCATATGATGATGATGATGAT 600
DB 1598 CTGTTCTTGTGATCACTGCAAGTTGGCGTTTTCATATGATGATGATGATGAT 1657

QY 601 TTGACAGCGCGCGCTCTGAGCGCGCGCGCTCTCCAGGGAAGTCTGAGCGCG 660
DB 1658 TTGACAGCGCGCGCTCTGAGCGCGCGCGCTCTCCAGGGAAGTCTGAGCGCG 1717

QY 661 AGAGAGCACTGGCAAGTCCGCGCACTGAAGATTACAGATACACACTCGTGC 720
DB 1718 AGAGAGCACTGGCAAGTCCGCGCACTGAAGATTACAGATACACACTCGTGC 1777

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DB 1778 GGTAAATCTTATACATCTTATTCATTTACCAATGCGGATGAACCAACGAGAT 1837

QY 781 GCGTCAGTTTCAGCTTCTTATACAGATTTGAGTACACTGCTGCTTTCATTT 840

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DB 2438 CAATTTGCTCAAAATTCGAATACGAATACGTTCTCCGATCATTAATTAAGATG 2497

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DB 2738 GCAATTTCTGCTGTATGAAAAAGCTGATTAACCGCAGGTAAATTTAAAGCTTAT 2797

QY 1741 ATTATGAACGCTTCCATGCTATGATGATTAATCTTATGAAGAAATTTAATTCCT 1800

DB 2798 ATTATGAACGCTTCCATGCTATGATGATTAATCTTATGAAGAAATTTAATTCCT 2857

QY 1801 TTTCCCTCTCTTTTTCAGCTGCTGAAGGATGCTGATTTGATATCTTATGAAGAAA 1860

DB 2858 TTTCCCTCTCTTTTTCAGCTGCTGAAGGATGCTGATTTGATATCTTATGAAGAAA 2917

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DB 2918 TTTATATTCCTGTTTTCCTATTTTCCAGTGTGAAGATTAACCGAGATGGGC 2977

QY 1921 TCCTGGAGCCGAGTGTATGTTCTTTTAAGTTCCTTAACGAGACACCTTCCAAATTTATG 1980
DB 2978 TCCCTGGAGCCGAGTGTATGTTCTTTTAAGTTCCTTAACGAGACACCTTCCAAATTTATG 3037
QY 1981 TTATGGCACTATTACCACTAGCTACTGAGCACTTCAAAATGAGCTTACTGATGACTG 2040
DB 3038 TTATGGCACTATTACCACTAGCTACTGAGCACTTCAAAATGAGCTTACTGATGACTG 3097
QY 2041 ACCAGTACTATTAATTTATGATCTGCTTTTGAACCCCTGTATACGCTGAGCACTTACT 2100
DB 3098 ACCAGTACTATTAATTTATGATCTGCTTTTGAACCCCTGTATACGCTGAGCACTTACT 3157
QY 2101 AGGTGACTTCAACAACTTGGATTCGAAATGAGCACTTACTGATGAGCACTG 2147
DB 3158 AGGTGACTTCAACAACTTGGATTCGAAATGAGCACTTACTGATGAGCACTG 3204

RESULT 2
AF338431 11475 bp DNA linear PLN 27-MAR-2001
LOCUS Aegilops tauschii starch branching enzyme ita gene, complete cds.
DEFINITION AF338431
ACCESSION AF338431
VERSION AF338431.1 GI:13447949

KEYWORDS
SOURCE
ORGANISM
Aegilops tauschii
Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Aegilops.
1 (bases 1 to 11475)
Rahman, S., Regina, A., Li, Z., Mukai, Y., Yamamoto, M.,
Kohar, Hashemi, B., Abrahams, S. and Morell, M.K.
Comparison of starch-branching enzyme genes reveals evolutionary
relationships among isoforms. Characterization of a gene for
starch-branching enzyme ita from the wheat genome donor Aegilops
tauschii
Plant Physiol. 125 (3), 1314-1324 (2001)

JOURNAL
MEDLINE
PUBMED
21140316
11244112
2 (bases 1 to 11475)
Rahman, S., Regina, A., Li, Z., Sharon, A. and Morell, M.K.
Direct Submission
Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Ross,
Canberra, ACT 2601, Australia
Location/Qualifiers
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NADTMRDYGWEIFLPNNADGSAIPHSRVIKIMDTSGVDSISAIKISVQAP
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ORIGIN
Query Match 98.9%; Score 2124; DB 8; Length 11475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2146; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 1 CGCGAGCTTCCACCCCGCGGACAGGTGCTCCCGCTTCATCGCTTCAATTAATA 60
DB 1058 CGCGAGCTTCCACCCCGCGGACAGGTGCTCCCGCTTCATCGCTTCAATTAATA 1117
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DB 1118 TCTCCATCACTCGGGTTCGGGCTGCATTTGGCGGGGTTGAGTGAATCTGGCGGA 1177
QY 121 CTGGCTGACTCAATCACTACGCGGGGATGCGAGCTTCCGGGTGCCGCGGACTCTTG 180
DB 1178 CTGGCTGACTCAATCACTACGCGGGGATGCGAGCTTCCGGGTGCCGCGGACTCTTG 1237
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DB 1418 GCTGTTCCTCCATTTGATCTCATGATGAGAGATTAAGGATCGGGCTTC 1477
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DB 1718 AGAGGACGACTTGGCAAGTCCGCGCAACTGAAGATTACAGTACACACTGTGTC 1777
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QY 840 TTGTTAGCTTGGCCCGCTGCTGCTTTGGGCACTGAAAAAATAGATGATGTGCAT 899

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QY 900 TCTAGAGAACTTCAACAACATATGACACCGTTGGGGTTTGGTCACTGTGTACAT 959
Db 1958 TCTAGCAAGAACTTCAACAACATATGACACCGTTGGGGTTTGGTCACTGTGTACAT 2017
QY 960 TGTATTTTCTGTCTGTAGTATACCTGAGATATCGAGAGCAAAACGGCGGAAGTAA 1019
Db 2018 TGTATTTTCTGTCTGTAGTATACCTGAGATATCGAGAGCAAAACGGCGGAAGTAA 2077
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QY 1560 GTTTTGGGGAAACACATTTGCTAAATTTGAAATGATTTGGGTATCTTCGGTGAATTCA 1619
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QY 1620 CAGATACAGGGAATACAGAGAAATTCGTCGCTTATGACCAACATGAGGTGATTTGA 1679
Db 2678 CAGATACAGGGAATACAGAGAAATTCGTCGCTTATGACCAACATGAGGTGATTTGA 2737
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QY 1860 ATTATATTTCTGTTTCCCTATTTTCCAGTGTGAAGATATCACTTACGAGAAATGG 1919
Db 2918 ATTATATTTCTGTTTCCCTATTTTCCAGTGTGAAGATATCACTTACGAGAAATGG 2977
QY 1920 CTCCCTGAGGCAATGATATGTTCTTTAAGTTCTTAAAGACACCTTCAATTTAT 1979
Db 2978 CT-CCTGAGGCAATGATATGTTCTTTAAGTTCTTAAAGTTCTTAAAGACACCTTCAATTTAT 3036

QY 1980 GTTAATGCTACTATTCACCAACTAGCTTACGACTTACCAATTAAGTACTGATACT 2039
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QY 2040 GACCACTTACTTAATTTATGATCTGGCTTTTGGCAACCTGTTACAGTCTGACGACTTAG 2099
Db 3097 GACCACTTACTTAATTTATGATCTGGCTTTTGGCAACCTGTTACAGTCTGACGACTTAG 3156
QY 2100 TAGGTGACTTCAACATTTGGAATTCGAATGACAGATCTATGACGAG 2147
Db 3157 TAGGTGACTTCAACATTTGGAATTCGAATGACAGATCTATGACGAG 3204

RESULT 3
AF064562 1852 bp DNA linear PLN 10-NOV-1998
LOCUS Hordeum vulgare cultivar Bomi starch branching enzyme Iia (sbeIIa)
DEFINITION gene, nuclear gene encoding plastid protein, partial cds.
ACCESSION AF064562
VERSION AF064562.1 GI:3851525
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 1852)
Sun, C., Sachish, P., Ahlandsberg, S. and Jansson, C.
The two genes encoding starch-branching enzymes Iia and Iib are
differentially expressed in barley
Plant Physiol. 118 (1), 37-49 (1998)
JOURNAL
MEDLINE
PUBMED
98404232
9733524
REFERENCE
2 (bases 1 to 1852)
Sun, C., Sachish, P., Ahlandsberg, S. and Jansson, C.
Direct Submision
Submitted (11-MAY-1998) Stockholm University, Biochemistry,
Stockholm S-10691, Sweden
LOCATION/Qualifiers
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exon

ORIGIN /number=2

Query Match 55.8%; Score 1197; DB 8; Length 1852;

Best Local Similarity 87.6%; Pred. No. 2.7e-281; Matches 1465; Conservative 1; Mismatches 168; Indels 38; Gaps 13;

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245 TCTCCATCACTCCCTCACTCGGTGGGCTCGGCTCGGCTGCTGATTTCCGCGG 304
98 CGGCTTGATGAGATCTGGGGGACTGGGCTGATCAATCACTAGCGGGGATGCGACGTT 157
305 CGTGTGATGAGATCTGGGCGACCGACTCGCTCGCTTGGCGGGADMTGGCGACGTT 364
158 CGCGATGTCGCGCGGACCTCTGATGATGGCGCGGCGCGGCTGCGA--GTGGCGCGGC 214
365 CGCGGTGTCGCGCGGACCGCTTGTGTGGCGCGGCGCGCGGAGAGCTGCGCGATC 424
215 CGGCTCGGAGCGGAGGGGCGGCGGACTTGGCTGCTCTCAGAGAGAGGACCTC 484
425 CGGCTCGGAGCGGAGGGGCGGCGGCTGAGCTTGGCTGCTCTCAGAGAGAGGACCTC 484
275 CTCTGATGAGCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 334
485 CTCTGATGAGCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 544
335 CTCTGCGCGCGGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 394
545 CTCTGCGACACACGCGCTGATGATGATGATGATGATGATGATGATGATGATGATG 604
395 ATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 453
605 ATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 664
454 CGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 512
665 CGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 724
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903 CTGAAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 962
749 TTACCAAAATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 807
963 TTACCAAAATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1022
808 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 867
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868 TGGGCACTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 927
1083 TGGGCACTGAAGAA-ACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1141
928 CGGTTGGGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 987

DB 1142 CTGTTT-TGGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 988 AGATATGAGAGCAACCGCGGAAATGATGATGATGATGATGATGATGATGATGATGATG 1047
DB 1201 AGATATGAGAGCAACCGCGGAAATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1048 ATCTTCAGAACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1107
DB 1261 ATCTTCAGAACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1108 TAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1167
DB 1321 TAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
QY 1168 AATATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1227
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QY 1228 CTTACCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1287
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QY 1288 CATCAAGAGACAAAGACTAGGAGACCACTATGATGATGATGATGATGATGATGATGATGATG 1347
DB 1501 CATCAAGAGACAAAGACTAGGAGACCACTATGATGATGATGATGATGATGATGATGATGATG 1560
QY 1348 TATGCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1407
DB 1561 TATGCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1408 AACTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1467
DB 1621 AACTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1468 TATGATTTTACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1526
DB 1681 TATGATTTTACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
QY 1527 GGAACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1586
DB 1741 GGAACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
QY 1587 CGAATGATTTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1638
DB 1801 TGAATCTTTTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1852

RESULT 4
AR340173 2853 bp DNA linear PAT 17-AUG-2003
LOCUS AR340173 Sequence 3 from patent US 6570066.
DEFINITION AR340173
ACCESSION AR340173
VERSION AR340173.1 GI:33731570
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2853)
AUTHORS Wilmittzer L., Kroger C., Luitcke S. and Lorz H.
TITLE Nucleotide sequences encoding enzymes that alter the carbohydrate
concentration and composition in plants
JOURNAL Patent: US 6570066-A 3 27-MAY-2003;
FEATURES
Location/Qualifiers
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ORIGIN
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Best Local Similarity 98.0%; Pred. No. 4.6e-48;
Matches 246; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 978 AGATACCTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1037

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Db 272 AGATACCTGAAGATATCCAGAGCAAAACCGCGAAGTGAACATGACAGAGGGGAGCTGCAG 331
QY 1038 AGAACTTCAATCTTTCAGAACCCGACTGAGGGCATTTGGGAAACAATCACTGATGGTGTAA 1097
Db 332 AAAAATTCAATCTTTCAGAACCCGACTGAGGGCATTTGGGAAACAATCACTGATGGTGTAA 391
QY 1098 CCAAAGAGTTAAGAACTAGTCTGTGGGGGAGAAACCGCGAGTTGTCCCAAAACGAGAG 1157
Db 392 CCAAAGAGTTAAGAACTAGTCTGTGGGGGAGAAACCGCGAGTTGTCCCAAAACGAGAG 451
QY 1158 ATGGGCGAGAAATATATACGAGATTGACCCCAACCTGAAGATTGTTGGAGCCATCTTGACT 1217
Db 452 ATGGGCGAGAAATATATACGAGATTGACCCCAACCTGAAGATTGTTGGAGCCATCTTGACT 511
QY 1218 ACCGGTAATGC 1228
Db 512 ACCGATACCGC 522

RESULT 5
TAU66376 2853 bp mRNA linear PLN 18-OCT-1996
LOCUS Triticum aestivum 1.4-alpha-D-glucan
DEFINITION 6-alpha-D-(1,4-alpha-D-glucanotransferase mRNA, complete cds.
ACCESSION U66376
VERSION U66376.1 GI:1620661
KEYWORDS Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 2853)
Kroege, C., Loerz, H. and Luetzelcke, S.
Direct Submission
Submitted (08-AUG-1996) University of Hamburg, Institute of General
Botany, Centre of Applied Molecular Biology, AMP II, Ohnhorststr.
18, Hamburg 22609, Germany
Location/Qualifiers
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QY 978 AGATACCTGAAGATATCCAGAGCAAAACCGCGAAGTGAACATGACAGAGGGGAGCTGCAG 1037
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Db 392 CCAAAGAGTTAAGAACTAGTCTGTGGGGGAGAAACCGCGAGTTGTCCCAAAACGAGAG 451
QY 1158 ATGGGCGAGAAATATATACGAGATTGACCCCAACCTGAAGATTGTTGGAGCCATCTTGACT 1217
Db 452 ATGGGCGAGAAATATATACGAGATTGACCCCAACCTGAAGATTGTTGGAGCCATCTTGACT 511
QY 1218 ACCGGTAATGC 1228
Db 512 ACCGATACCGC 522

RESULT 6
BT008928 2549 bp mRNA linear PLN 20-JUN-2003
LOCUS Triticum aestivum clone wdel.f.pk002.98.fis, full insert mRNA
DEFINITION sequence.
ACCESSION BT008928
VERSION BT008928.1 GI:32128479
KEYWORDS FLI CDNA.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 2549)
Tingey, S.V., Wolters, P., Powell, W., Dolan, M., Miao, G.-H.,
Carlier, N.R., Hanafey, M.K. and Hainey, C.F.
Direct Submission
Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA
Location/Qualifiers
FEATURES
source 1..2549
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ORIGIN
Query Match 11.1%; Score 238.2; DB 8; Length 2549;
Best Local Similarity 96.8%; Pred. No. 6.7e-47;
Matches 243; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 978 AGATACCTGAAGATATCCAGAGCAAAACCGCGAAGTGAACATGACAGAGGGGAGCTGCAG 1037
Db 283 AGATACCTGAAGATATCCAGAGCAAAACCGCGAAGTGAACATGACAGAGGGGAGCTGCAG 342
QY 1038 AGAACTTCAATCTTTCAGAACCCGACTGAGGGCATTTGGGAAACAATCACTGATGGTGTAA 1097
Db 343 AGAACTTCAATCTTTCAGAACCCGACTGAGGGCATTTGGGAAACAATCACTGATGGTGTAA 402
QY 1098 CCAAAGAGTTAAGAACTAGTCTGTGGGGGAGAAACCGCGAGTTGTCCCAAAACGAGAG 1157
Db 403 CCAAAGAGTTAAGAACTAGTCTGTGGGGGAGAAACCGCGAGTTGTCCCAAAACGAGAG 462
QY 1158 ATGGGCGAGAAATATATACGAGATTGACCCCAACCTGAAGATTGTTGGAGCCATCTTGACT 1217
Db 463 ATGGGCGAGAAATATATACGAGATTGACCCCAACCTGAAGATTGTTGGAGCCATCTTGACT 522
QY 1218 ACCGGTAATGC 1228
Db 523 ACCGATACCGC 533
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RESULT 7
LOCUS AF338432
DEFINITION Triticum aestivum starch branching enzyme I1a variant mRNA,
complete cds.
ACCESSION AF338432
VERSION AF338432.1 GI:13447951
KEYWORDS Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
DEFINITION Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 2726)
AUTHORS Rahman, S., Regina, A., Li, Z., Mukai, Y., Yamamoto, M.,
Kosar-Hademi, B., Abrahams, S. and Morell, M.K.
REFERENCE Comparison of starch-branching enzyme genes reveals evolutionary
relationships among isoforms. Characterization of a gene for
starch-branching enzyme I1a from the wheat genome donor Aegilops
tauschii.
JOURNAL Plant Physiol. 125 (3), 1314-1324 (2001)
MEDLINE 21140316
PubMed 11244112
REFERENCE 2 (bases 1 to 2726)
AUTHORS Rahman, S., Regina, A., Li, Z., Abrahams, S. and Morell, M.K.
TITLE Direct Submission
JOURNAL Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Ross,
Canberra, ACT 2601, Australia
LOCATION/Qualifiers
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124. 2430
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Query Match 10.9%; Score 235; DB 8; Length 2726;
Best Local Similarity 96.0%; Pred. No. 4.1e-46;
Matches 241; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

2y 978 AGATACCTCGAAGATATTCGAGGCAACCGCGGAAGTGAACATGACAGGGGGGACGCGG 1037
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2y 1038 AGAACTCAATCTTCAGAACGCACTCAGGCACTTGCGAAACAATCATCTGATGTGTA 1097
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3b CCAAGGAGTTAAGAACTAGTGTGGGGGAGAAACCGCGAGTTGTCACAAAACGAGAG 379
2y 1158 ATGGCAGAAAATATTCGAGATTGACCCCAACTGAAGATTTTCGAGAGCATCTTGACT 1217

Db 380 ATGGCAGAAAATATTCGAGATTGACCCCAACTGAAGATTTTCGAGAGCATCTTGACT 439
Qy 1218 ACCGGTAATGC 1228
Db 440 ACCGATACAGC 450

RESULT 8
LOCUS TASB2
DEFINITION T.aestivum mRNA for starch branching enzyme II.
ACCESSION Y11282
VERSION Y11282.1 GI:1865343
KEYWORDS 1,4-alpha-glucan branching enzyme; sbe2 gene; starch branching
enzyme II.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
DEFINITION Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1
AUTHORS Nair, R.B., Baga, M., Scoles, G.J., Kartha, K.K. and Chibbar, R.N.
TITLE Isolation, characterization and expression analysis of a starch
branching enzyme II cDNA from wheat
JOURNAL Plant Sci.
2 (bases 1 to 2970)
AUTHORS Chibbar, R.N.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology
Institute, National Research Council of Canada, 110 Gymnasium
place, Saskatoon, Saskatchewan S7N 0W9, CANADA
LOCATION/Qualifiers
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1. 2970
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151. 2622
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polYA_site	/gene="sbe2"	2948	/gene="sbe2"
Query Match	10.9%	Score 235; DB 8; Length 2970;	
Best Local Similarity	96.0%	Pred. No. 4.2e-46;	
Matches 241; Conservative	0;	Mismatches 10; Indels 0; Gaps 0;	
Db	978	AGATACCTGAAGATATCGAGAGCAAAACGCGGAGATGACATGACAGGGGGACTGCAG	10377
Db	392	AGATACCTGAAGATATCGAGAGCAAAACGCGGAGATGACATGACAGGGGGACTGCAG	451
Qy	1038	AGAACTTCAATCTTCAGAACCCGACTCAGGGCATTTGTGAAAACAATCACTGATGCTTAA	1097
Db	452	AAAACTGAATCTTCAGAACCCGACTCAGGGCATTTGTGAAAACAATCACTGATGCTTAA	511
Qy	1098	CCAAAGGACTTAAAGAACTAGTCGTGGGGGGAAGAAACCGCGATTTGCCCAAAACGAGAG	1157
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Qy	1158	ATGGGCAAAAAATATACAGAGATTGACCCCAAGCACTGAAGATTTTTCGAGCCATCTTGACT	1217
Db	572	ATGGGCAAAAAATATACAGAGATTGACCCCAAGCACTGAAGATTTTTCGAGCCATCTTGACT	631
Qy	1218	ACCGGTAATGC 1228	
Db	632	ACCGTAACGC 642	
RESULT 9	AF286319	2970 bp	mRNA linear PLN 14-MAR-2003
LOCUS	AF286319	Triticum aestivum starch branching enzyme 2 (Sbe2)	mRNA, complete
DEFINITION	cds		
ACCESSION	AF286319	GI:11037533	
VERSION	AF286319.1		
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
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FEATURES			
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ORIGIN
Query Match      10.9%; Score 233.4; DB 8; Length 2970;
Batch Local Similarity 95.6%; Pred. No. 1e-45;
Matches 240; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Dy 390 AGATACCTGAAGACATCGAGAGGCAACCGCTGAATGAACATGACAGGGGGGACTGCG 449
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Dy 1038 AGAACTTCAATCTTCAGAACCGACTCAGGGCATTTGGGAAACAATCATGATGCTGTA 1097
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Dy 450 AAAAATTGATCTCTCGAACCCGACTAAGGCATTGGAAACAATCATGATGCTGTA 509
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Dy 1098 CCAAGAGGATTAAGAACTAGTCGTGGGGGAGAAACGCGAGTGTCCCAAAACAGAG 1157
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Dy 510 CCAAGAGGATTAAGAACTAGTCGTGGGGGAGAAACCGAGTGTCCCAAAACAGAG 569
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Dy 1158 ATGGCGAGAAATATAGAGATTGACCCCACTGAAAGATTTTCGAGGACATCTTGACT 1217
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Dy 570 ATGGCGAGAAATATAGAGATTGACCCCACTGAAAGATTTTCGAGGACATCTTGACT 629
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Db 1218 ACCGGTAATGC 1228
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Db 630 ACCGATACAGC 640

RESULT 10
AF064560 2554 bp mRNA PLN 03-NOV-1998
LOCUS
DEFINITION Hordeum vulgare cultivar Bomi starch branching enzyme Iia (beta)
ACCESSION AF064560
VERSION
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Strepotophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 2554)
Sun,C., Sathish,P., Ahlandsberg,S. and Jansson,C.
The two genes encoding starch-branching enzymes Iia and Iib are
differentially expressed in barley
Plant Physiol. 118 (1), 37-49 (1998)
JOURNAL
MEDLINE
98404232
PUBMED
9739324
2 (bases 1 to 2554)
Sun,C., Sathish,P., Ahlandsberg,S. and Jansson,C.
Direct Submission
Submitted (11-MAY-1998) Stockholm University, Biochemistry,
Stockholm S-10691, Sweden
Location/Qualifiers
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/mol_type="mRNA"

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PHGSRVKIRMDTPSGVSDISAWTKFSVQAGBEIPENGIYYDPEEEKYFQHPQPKR
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HATVTFAPSSRFPTPEDKSLIDRAHELGLVMDIVSHSSNNTLDLNGFDCTDTH
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ORIGIN

Query Match 9.4%; Score 201.4; DB 8; Length 2554;
Best Local Similarity 93.0%; Pred. No. 6.6e-38;
Matches 211; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

2Y 1002 AACGCGGGAAGTGAACATGACAGGGGGAGCTGCAGAGAACTTCATCTTCAGAACCA 1061
5 AGATGGCGGAAGTGAACATGACAGGGGGAGCTGCAGAGAACTTCATCTTCAGAACCA 64
2Y 1062 CTCAGGGCATTGTGGAACAAATCACTGATGCTGTAACCAAGAGTTAAGAACTAGTGC 1121
65 CTCAGGGTATGTCGGAACAAATCACTGATGCTGTAACCAAGAGTTAAGAACTAGTGC 124
2Y 1122 TGGGGGGAAGACCGCGAGTTTCCCAAAACGAGAGTGGGAGAAATATCGGATTCG 1181
125 TTGGGGGGAAGACCGCGAGTTTCCCAAAACGAGAGTGGGAGAAATATCGGATTCG 184
2Y 1182 ACCGAACCTGAAGATTTCCGAGCCATCTGATACCGGATATGC 1228
185 ACCGAACCTGAAGATTTCCGAGCCATCTGATACCGGATATGC 231

RESULT 11

AY357072 3094 bp DNA linear PLN 02-SEP-2003
LOCUS Triticum aestivum cultivar Yumai-18 starch branching enzyme Ila
DEFINITION (SbeIIa) gene, promoter region and partial cds.
ACCESSION AY357072
VERSION AY357072.1 GI:34329814

SOURCE

ORGANISM Triticum aestivum (bread wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.

1 (bases 1 to 3094)
Miao,H.M., Han,J.F. and Fleming,J.E.
Investigation of endosperm-specific promoters in wheat

JOURNAL Unpublished
2 (bases 1 to 3094)

REFERENCE Miao,H.M., Han,J.F. and Fleming,J.E.
AUTHORS Direct Submission
TITLE Submitted (31-Jun-2003) Institute of Biotechnology, Henan Academy
JOURNAL of Agricultural Sciences, No.1 Nongye Road, Zhengzhou, Henan
Province 450002, China

FEATURES
source 1..3094

ORIGIN

Query Match 6.9%; Score 149; DB 8; Length 3094;
Best Local Similarity 100.0%; Pred. No. 4.5e-25;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCAGCTTCACCCCGCCGACACCTGTGTCCTCCCTTCATCGCTTCATTAATA 60
DB 2946 CGCCAGCTTCACCCCGCCGACACCTGTGTCCTCCCTTCATCGCTTCATTAATA 3005
QY 61 TCTCCATCACTCGGGTTCGCGCTGCTTCGCGCGGGTGTAGAGATTCGGCGCA 120
DB 3006 TCTCCATCACTCGGGTTCGCGCTGCTTCGCGCGGGTGTAGAGATTCGGCGCA 3065
QY 121 CTGGCTGACTCACTCACTACGCGGGGATG 149
DB 3066 CTGGCTGACTCACTCACTACGCGGGGATG 3094

RESULT 12

OSUN00286/c 159683 bp DNA linear HTG 14-NOV-2003
LOCUS Oryza sativa (japonica cultivar-group) chromosome 4 clone
DEFINITION OSUNBa0042115, *** SEQUENCING IN PROGRESS ***; 11 ordered pieces.
ACCESSION AL731641
VERSION AL731641.3 GI:32490295
KEYWORDS HTG; HTGS PHASE2.

SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Peng,Q., Zhang,Y., Hao,P., Wang,S., Fu,G., Huang,Y., Li,Y., Zhu,J.,
Liu,Y., Hu,X., Jia,P., Zhang,Y., Zhao,Q., Ying,K., Yu,S., Tang,Y.,
Weng,Q., Zhang,L., Lu,Y., Mu,J., Lu,Y., Zhang,L.S., Yu,Z., Fan,D.,
Liu,X., Lu,T., Li,C., Wu,Y., Sun,T., Lei,H., Li,T., Hu,H., Guan,J.,
Wu,M., Zhang,R., Zhou,B., Chen,Z., Chen,L., Jin,Z., Wang,R.,
Yin,H., Cai,Z., Ren,S., Lv,G., Gu,W., Zhu,G., Tu,Y., Hu,Q.,
Zhang,Y., Chen,J., Kang,H., Chen,X., Shao,C., Sun,Y., Hu,Q.,
Zhang,X., Zhang,W., Wang,L., Ding,C., Sheng,H., Gu,J., Chen,S.,
Ni,L., Zhu,F., Chen,W., Lan,L., Lai,Y., Cheng,Z., Gu,M., Jiang,J.,
Li,J., Hong,G., Xue,Y. and Han,B.
Sequence and analysis of rice chromosome 4
NATURE 420 (6913), 316-320 (2002)
JOURNAL MEDLINE
PUBMED 2237377
12447439
2 Fu,G., Wang,S.Y., Ren,S.X., Lv,G., Lin,W., Gu,W.Q., Zhu,G.F.,

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (04-MAY-2002) Han Bin, National Center for Gene Research,
Chinese Academy of Sciences, 500# Cao Bao Road, Shanghai 200233.
CHINA. E-mail enquiries: dhanncgr.ac.cn. Clone requests:
dhanncgr.ac.cn
Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC
clone OSJNBa0042115.
On Jul 9, 2003 this sequence version replaced gi:21912624.
Web site: <http://www.ncgr.ac.cn>
----- Summary Statistics -----
Assembly program: phrap

NOTE: This is a PHASE2 sequence. Gaps are shown by 200n. Gens were
identified by a combination of several methods: Gene prediction
programs including Fgenesh (<http://www.softberry.com/>), genescan
(<http://CCR-081.mil.edu/GENSCAN.html>), GenemarkHMM
(<http://genemark.biology.gatech.edu/Genemark/>), tRNAscan-SE (Sean
Eddy <http://genome.wustl.edu/eddy/tRNAscan-SE/>), searches of the
complete sequence against NCBI non-redundant protein database (nr)
(<ftp://ncbi.nlm.nih.gov/blast/db>) and the EST database at NCGR.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 9353: contig of 9353 bp in length
* 9354 9553: gap of 200 bp
* 47134: contig of 37581 bp in length
* 47135 47334: gap of 200 bp
* 47335 51470: contig of 4136 bp in length
* 51471 51670: gap of 200 bp
* 51671 62557: contig of 10887 bp in length
* 62558 62757: gap of 200 bp
* 62758 82635: contig of 19878 bp in length
* 82636 82835: gap of 200 bp
* 82836 88339: contig of 5504 bp in length
* 88340 88539: gap of 200 bp
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* 102631 102830: gap of 200 bp
* 102831 122977: contig of 20147 bp in length
* 122978 123177: gap of 200 bp
* 123178 135293: contig of 12116 bp in length
* 135294 135493: gap of 200 bp
* 135494 142342: contig of 6849 bp in length
* 142343 142542: gap of 200 bp
* 142543 159683: contig of 17141 bp in length.
Location/Qualifiers

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source

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FN JP 1998004970-A/2
 PD 13-JAN-1998
 PF 24-JUN-1996 JP 1996162983
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 C12N15/09,A01H5/00,C07H21/04,C12N5/10,C12N9/10,(C12N15/09, PC
 C12R1:91),
 PC (C12N5/10,C12R1:91),(C12N9/10,C12R1:19);
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 CC topology: Linear;
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 FT CDNA library'
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 Best Local Similarity 76.3%; Pred. No. 7e-22;
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 DB 162 GGCGAAGTGAACATGACAGGGGGGACTGCAGAGAACTTCATCTTCAGAACCGACTCA 221
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 DB 282 GGATTAACCGAGATTATCCACCAACGAGATGCGGAGAAATATCAAAATTGACCC 341
 QY 1186 AACACTGAAGATTTTCGAGCCATCTTGACTACCGGTA 1224
 DB 342 AATGCTGAAGATTTTCGAGCCATCTTGACTACCGGTA 380

RESULT 14

LOCUS E14723 3015 bp DNA linear PAT 28-JUL-1999
 DEFINITION Rice mRNA for branching enzyme-4, complete cds.
 ACCESSION E14723
 VERSION E14723.1 GI:5709406
 KEYWORDS JP 1998004970-A/1.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.

REFERENCE

1 (bases 1 to 3015)
 Baba,T., Kawasaki,T. and Ichikawa,N.
 NEW RICE GENE FOR STARCH-BRANCHING ENZYME
 Patent: JP 1998004970-A 1 13-JAN-1998;
 MITSUI GYOSAI SHOKUBUTSU BIO KENKUSHO:KT, MITSUI PETROCHEM IND LTD
 OS Oryza sativa (rice)
 PN JP 1998004970-A/1

COMMENT

PD 13-JAN-1998
 PF 24-JUN-1996 JP 1996162983
 PI BABA TADASHI, KAWASAKI TSUTOMU, ICHIKAWA NORIO PC
 C12N15/09,A01H5/00,C07H21/04,C12N5/10,C12N9/10,(C12N15/09, PC
 C12R1:91),
 PC (C12N5/10,C12R1:91),(C12N9/10,C12R1:19);

CC strandedness: Double;
 CC topology: Linear;
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Query Match 6.3%; Score 135.8; DB 6; Length 3015;
 Best Local Similarity 76.3%; Pred. No. 7.5e-22;
 Matches 167; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1006 GGCGAAGTGAACATGACAGGGGGGACTGCAGAGAACTTCATCTTCAGAACCGACTCA 1065
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 QY 1186 AACACTGAAGATTTTCGAGCCATCTTGACTACCGGTA 1224
 DB 629 AATGCTGAAGATTTTCGAGCCATCTTGACTACCGGTA 667

RESULT 15

LOCUS AB023498 3015 bp mRNA linear PLN 04-AUG-1999
 DEFINITION Oryza sativa mRNA for starch branching enzyme rbe4, complete cds.
 ACCESSION AB023498
 VERSION AB023498.1 GI:5689137
 KEYWORDS starch branching enzyme rbe4.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.

REFERENCE

1 (sites)
 Mizuno,K., Tachibana,M., Kobayashi,E., Kawasaki,T., Funane,K.,
 Kobayashi,M. and Baba,T.
 Molecular cloning and expression analysis of a novel member of
 starch branching enzyme isoform in developing rice seeds
 unpublished

JOURNAL

2 (bases 1 to 3015)
 Mizuno,K. and Baba,T.
 Direct Submission
 Submitted (09-FEB-1999) Kouichi Mizuno, University of Tsukuba,
 Institute of Agricultural and Forest Engineering, 1-1-1 Tennoudai,
 Tsukuba, Ibaraki 305-8572, Japan
 (E-mail:koumomo@tsukuba.ac.jp, Tel:81-298-53-4656,
 Fax:81-298-55-2203)

FEATURES

source Location/Qualifiers
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ORIGIN

Query Match 6.3%; Score 135.8; DB 8; Length 3015;
Best Local Similarity 76.3%; Pred. No. 7.5e-22;
Matches 167; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 1006 GCGGAACTGAACATGACAGGGGAGCTGACAGAAACTTCAATCTTCAGAACCGACTCA 1065
DB 449 GCGAAGAACCAATGAAGCTGTGGCTGAAGCAAACTTGAATCTTCAGAACTGATTC 508
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DB 509 AGACATTAGGAAATGTGACTGAGGGTGTGATCAAAAGATGCTGATGAACCAACTGTG 568
QY 1126 GGAAGAACCGGAGCTGTCCCAAAACCAAGAGATGGGCAAGAAATATACGAGATTGACCC 1185
DB 569 GGATTAACCGAGTATCCCAACCAAGAGATGGGCAAGATATACCAAAATTGACCC 628
QY 1186 AACACTGAAGATTTCGAGAGCCATCTTGACTACCGGTA 1224
DB 629 AATGCTGGAAGATTTCGGAACCATCTTGACTACCGATA 667

Search completed: April 10, 2004, 10:02:19
Job time : 8425.29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

DM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 01:51:55 ; Search time 840.046 Seconds
(without alignment)
10857.595 Million cell updates/sec

Title: US-09-508-377-10_COPY_1058_3204

Perfect score: 2147
Sequence: 1 cgcgcagcttcacaccccgcc.....tcgacatcattgaccagag 2147

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2127	99.1	11473	2	AA34650 Starch br
2	2124	98.9	11475	5	Aah78338 Nucleotid
3	235	10.9	2726	5	Aah78337 Nucleotid
4	177.6	8.3	226	5	Aah78351 Nucleotid
5	164.2	7.6	217	5	Aah78353 Nucleotid
6	159.2	7.4	228	5	Aah78352 Nucleotid
7	135.8	6.3	3015	2	AAV05639 Rice type
8	117.8	5.5	2655	7	ADA71289 Rice gene
9	116	5.4	2304	9	ADC08218 Rice DNA
10	84.4	3.9	2968	5	Aah78342 Nucleotid
11	84.4	3.9	3039	6	ABK15494 Wheat sta
12	82.2	3.8	3962	5	Aah78341 Partial s
13	82.2	3.8	8381	5	Aah78343 Partial s
14	79.4	3.7	2919	5	AAQ73750 Rice star
15	78.6	3.7	2307	9	ADC07807 Rice DNA
16	73.8	3.4	23449	3	AAZ35393 Maize amy
17	61.6	2.9	2640	2	AAV70961 DNA encod
18	59.8	2.8	2577	6	AB212532 Arabidops
19	59.8	2.8	2715	3	AAc45939 Arabidops
20	58.8	2.8	3331	2	AA142632 Class A s
21	58.4	2.7	3090	2	AAV38720 Full leng
22	58.4	2.7	2087	2	AA169737 Corn star
23	58.4	2.7	2165	2	AA169736 Corn star

24	58.4	2.7	2665	2	AA169729 Placmid p
25	58.4	2.7	2725	2	AAV29757 Zea mays
26	58.4	2.7	2913	2	AAV38719 Full leng
27	58.2	2.7	2531	2	AA17267 Class A s
28	58.2	2.7	2563	5	ABK50301 Potato cd
29	58.2	2.7	2576	2	AA172636 Class A s
30	58.2	2.7	2578	2	AA172631 Class A s
31	58.2	2.7	3033	2	AA142630 Class A s
32	58.2	2.7	3074	2	AA142630 Class A s
33	57.2	2.7	262	5	AA169587 Nucleotid
34	56.6	2.6	3003	2	AA142634 Class A s
35	55	2.6	2418	6	AB213067 Arabidops
36	55	2.6	2418	7	ADA68438 Arabidops
37	55	2.6	2529	2	AA142637 Class A s
38	53.8	2.5	507	2	AA169733 Corn star
39	52.6	2.4	349	3	AA167270 Pinus rad
40	52.6	2.4	481	3	AA167264 Pinus rad
41	50.2	2.3	335913	5	AA161371 Soybean 2
42	50.2	2.3	335913	5	AA161372 Soybean 2
43	47.8	2.2	2975	2	AA142635 Class A s
44	45.2	2.1	282	6	AB173359 Corn tass
45	45.2	2.1	2000	7	ADA71938 Rice gene

ALIGNMENTS

RESULT 1	AA34650	AA34650 standard; DNA, 11473 BP.
ID	AA34650	
AC	AA34650	
XX		
DT	17-OCN-2003 (revised)	
DT	05-JUL-1999 (first entry)	
XX		
DE	Starch branching enzyme II (SBE II) gene sequence.	
XX		
KW	Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBS;	
KW	starch branching enzyme; starch soluble synthase; debbranching enzyme;	
KW	endosperm; wheat; barley; granule-bound synthase; glucrenn; starch;	
KW	grain softness protein I; bacterial isomylase; glycogen synthase;	
KW	WBBE I-D4 gene; ss.	
XX		
OS	Aegilops tauschii.	
XX		
PN	W09914314-A1.	
XX		
PD	25-MAR-1999.	
XX		
PF	11-SEP-1998; 98WO-AU000743.	
XX		
PR	12-SEP-1997; 97AU-00009108.	
PR	20-MAR-1998; 98AU-00002509.	
XX		
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
PA	(AUSU) UNIV AUSTRALIAN NAT.	
PA	(GOOD-) GOODMAN FIELDER LTD.	
PA	(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.	
XX		
PI	L1 Z, Morell M, Rahman S;	
XX		
DR	WPI; 1999-229525/19.	
XX		
PT	New isolated cereal plant enzyme genes used for, e.g. expression of	
PT	antisense sequences of granule bound synthase.	
XX		
PS	Claim 8; Page 75-81; 171pp; English.	
XX		
CC	The invention relates to a novel enzyme of starch biosynthetic pathway in	
CC	a cereal plant, where the enzyme is selected from starch branching enzyme	
CC	(SBE) I, SBE II, starch soluble synthase (SSS) I, and debbranching enzyme	
CC	(DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of	

rice or maize. The methods and products can be used for targeting expression specifically to the endosperm of the seeds of cereal plants such as wheat or barley. They can be used for the expression of e.g. antisense sequences of granule-bound synthase (GBSS), SBE II, low mol. wt. glutenin, grain softness protein I, bacterial isomylase, bacterial glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be used for modifying the characteristics of starch produced by a plant. The present sequence represents the SBE II gene sequence. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 11473 BP; 3096 A; 2263 C; 2423 G; 3691 T; 0 U; 0 Other;

Query Match 99.1%; Score 2127; DB 2; Length 11473;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2147; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

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QY 1 CCGCAGCTTCACCCCGCGGACAGCTTGCCTCCCTTCTCATCGCTTCTCATTTATA 60
DB CCGCAGCTTCACCCCGCGGACAGCTTGCCTCCCTTCTCATCGCTTCTCATTTATA 1117
QY 61 TCTCCACTCGGGGTTCCGGCGTGCAATTCCGGCGGGGTTAGTGAATCGGGCGA 120
DB TCTCCACTCGGGGTTCCGGCGTGCGGGGATGGCGAGTTCCGGGTCGCGCACTCG 1237
QY 1118 TCTCCACTCGGGGTTCCGGCGTGCAATTCCGGCGGGGTTAGTGAATCTGGGCGA 1177
DB 1118 TCTCCACTCGGGGTTCCGGCGTGCGGGGATGGCGAGTTCCGGGTCGCGCACTCG 1237
QY 121 CTGCGTCACTCAATCACTACGCGGGGATGGCGAGCTTCGCGGTGCCGCGCACTCG 180
DB 1178 CTGCGTCACTCAATCACTACGCGGGGATGGCGAGTTCCGGGTCGCGCACTCG 1237
QY 181 GTGTGGCGGGGCGCGGCTGGAAGTGGCGGCGCGGCTCGAGCGGAGGGGCGGCG 240
DB 1238 GTGTGGCGGGGCGCGGCTGGAAGTGGCGGCGCGGCTCGAGCGGAGGGGCGGCG 1237
QY 241 ACTTGGCGGCTGCTCCTCAGAGAGAGAGACTCTCTCGAGCGCTCGCTCGCAT 300
DB 1298 ACTTGGCGGCTGCTCCTCAGAGAGAGAGACTCTCTCGAGCGCTCGCTCGCAT 1357
QY 301 CTCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 1358 CTCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1417
QY 361 GCTGTTCCCAATTGATCTCCATGAGTGAAGAGATGCTGGATTAGCGCATTCGCGCTTC 420
DB 1418 GCTGTTCCCAATTGATCTCCATGAGTGAAGAGATGCTGGATTAGCGCATTCGCGCTTC 1477
QY 421 CTGAACCTGATTTTTTCCCCCGGGGAAATGCGTTAGTGTCAACCAAGGCGCTGAGTT 480
DB 1478 CTGAACCTGATTTTTTCCCCCGGGGAAATGCGTTAGTGTCAACCAAGGCGCTGAGTT 1537
QY 481 ACCACGGCTTGAATCATCTCGTTTCTCTGATATATATATTTCTATTTCTTCTC 540
DB 1538 ACCACGGCTTGAATCATCTCGTTTCTCTGATATATATATTTCTATTTCTTCTC 1597
QY 541 CTGTTCTTGTGTAAGTGAAGTTGGCGTTTTTCTATTTAGTCAATCTTGTGATT 600
DB 1598 CTGTTCTTGTGTAAGTGAAGTTGGCGTTTTTCTATTTAGTCAATCTTGTGATT 1657
QY 601 TTGCAAGCGCGGCTGAGCGCGCGGCGCTCGAGGGAAGTCTCTGCTGCTGCAAGCG 660
DB 1658 TTGCAAGCGCGGCTGAGCGCGCGGCGCTCGAGGGAAGTCTCTGCTGCTGCAAGCG 1717
QY 661 AGAGAGCACTTGGCAAGTCCGGCGCAACCTGAAGATTACAGGTACACACACTCGTCC 720
DB 1718 AGAGAGCACTTGGCAAGTCCGGCGCAACCTGAAGATTACAGGTACACACACTCGTCC 1777
QY 721 GGTAAATCTTCATCAATCTGTTATTCATTAACAAATCCGAGTGAACCAACAGGAT 780
DB 1778 GGTAAATCTTCATCAATCTGTTATTCATTAACAAATCCGAGTGAACCAACAGGAT 1837
QY 781 GCGTCAGGTTTCAGAGCTTCTTCATGAGCATTTGAGCATCTGCACTGCTTGTTCATT 840
DB 1838 GCGTCAGGTTTCAGAGCTTCTTCATGAGCATTTGAGCATCTGCACTGCTTGTTCATT 1897
QY 841 TGTTAGCTTGGCCCGGCTGCTGCTTGGGCACTGAAAAAATCAGATGATGTGATT 900
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DB 1898 TGTTAGCTTGGCCCGGCTGCTGCTTGGGCACTGAAAAATCAGATGATGTGATT 1957
QY 901 CTAGCAAGACTTCACCAATATATGACCGGTTTGGGGTTTGGTCAAGTCTGCTCAATT 960
DB CTAGCAAGACTTCACCAATATATGACCGGTTTGGGGTTTGGTCAAGTCTGCTCAATT 1958
QY 961 GCTATTTTCTGCTGATGATACCTGAAGATATCGAGAGCAACCGCGGAATGAAAT 1020
DB GCTATTTTCTGCTGATGATACCTGAAGATATCGAGAGCAACCGCGGAATGAAAT 2017
QY 1021 GACAGGGGGGACTGAGAGAAAATCTTCAATCTTCAAGACCGACTCAGGGCATTTGAAAC 1080
DB 2018 GCTATTTTCTGCTGATGATACCTGAAGATATCGAGAGCAACCGCGGAATGAAAT 2077
QY 1081 AATCACTGATGATGATACCAAGAGTTAAGGAACTAGTCTGAGGGGAGAAACCGGAGT 1140
DB 2138 AATCACTGATGATGATACCAAGAGTTAAGGAACTAGTCTGAGGGGAGAAACCGGAGT 2197
QY 1141 TGTCCAAAACCGAGAGATGGGCAAGAAATATACAGATTGACCCCAACTGAAAGATT 1200
DB 2198 TGTCCAAAACCGAGAGATGGGCAAGAAATATACAGATTGACCCCAACTGAAAGATT 2257
QY 1201 TCGAGCCATCTTACTACCGGT-----ATGCTTACCGGCTGCTTGGCTCAT 1250
DB 2258 TCGAGCCATCTTACTACCGGTAAATGCTTACCAATGCTTACCGGCTGCTTGGCTCAT 2317
QY 1251 TTGAATTAAGGCTTCTTATCATGCAAAATTTGGGGAATCAAGAGACAAAGACTAGG 1310
DB 2318 TTGAATTAAGGCTTCTTATCATGCAAAATTTGGGGAATCAAGAGACAAAGACTAGG 2377
QY 1311 ACCACATTTTCATACAGATCCCTTGTGCTGAGAAATGCTGGAAGTAAATGATTA 1370
DB 2378 ACCACATTTTCATACAGATCCCTTGTGCTGAGAAATGCTGGAAGTAAATGATTA 2437
QY 1371 TTGATGCTCAATTTGCTCAAAATTTGCATACGAATACTGCTCCGATCATTAAT 1430
DB 2438 TTGATGCTCAATTTGCTCAAAATTTGCATACGAATACTGCTCCGATCATTAAT 2497
QY 1431 AAAGGTGGCAAACTGAGAAATGAGTGAATGGGTATAGATTTTACTTCTAATTC 1490
DB 2498 AAAGGTGGCAAACTGAGAAATGAGTGAATGGGTATAGATTTTACTTCTAATTC 1557
QY 1491 CTCTACCAAAATCTCAGGGGGGAAATCTACAGTTGGGAACTTAATTTCTATCTTGT 1550
DB 2558 CTCTACCAAAATCTCAGGGGGGAAATCTACAGTTGGGAACTTAATTTCTATCTTGT 2617
QY 1551 GGCTTTTGTGTTGGGGAACACATTTGCTAATTCGAATGATTTTGGGTATACCTCG 1610
DB 2618 GGCTTTTGTGTTGGGGAACACATTTGCTAATTCGAATGATTTTGGGTATACCTCG 2677
QY 1611 TGGATTCAACAGATCAGGGAATCAAGAGAAATTCGCTGCTAATGACCAATGAAG 1670
DB 2678 TGGATTCAACAGATCAGGGAATCAAGAGAAATTCGCTGCTAATGACCAATGAAG 2737
QY 1671 TGGATTGAAAGCAATTTCTGAGTTATGAAAAAGCTTGAATTTACCCGCAAGTAAAT 1730
DB 2738 TGGATTGAAAGCAATTTCTGAGTTATGAAAAAGCTTGAATTTACCCGCAAGTAAAT 2797
QY 1731 AAGCTTTATTTATGAAGACGCTCCATAGTCTAATTTGCATCTTATTAAGAAAAAT 1790
DB 2798 AAGCTTTATTTATGAAGACGCTCCATAGTCTAATTTGCATCTTATTAAGAAAAAT 2857
QY 1791 TAATCCGTTTCCCTCTCTTTTTCAGAGCTGAAGGATAGTCTAATTTGCATCTT 1850
DB 2858 TAATCCGTTTCCCTCTCTTTTTCAGAGCTGAAGGATAGTCTAATTTGCATCTT 2917
QY 1851 TATAAGAAATTTATATCTGTTTCCCTATTTTCAAGTCTGAAGGATACCTTAAC 1910
DB 2918 TATAAGAAATTTATATCTGTTTCCCTATTTTCAAGTCTGAAGGATACCTTAAC 2977
QY 1911 CAGATGGGCTCCCGAGCGGATGTTATGTTCTTTAAGTTCTTAAGGACACCTTC 1970
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2978 GAGNATGGGCTCCCTGGAGCGGCATGTTATGTTCTTTAAGTTCCTTAACGAGACACCTTC 3037
1971 CAATTTTGTATATGTCATATTCACCACTAGCTTACGGAATTCATTAATAGCTTA 2030
3038 CAATTTATGTTATGTCATATTCACCACTAGCTTACGGAATTCATTAATAGCTTA 3097
2031 CTGAAATCTGACGACCTTACTATTAATTTATGATCTGCTTTGACACCTGTTACAGCTCG 2090
3098 CTGAATCTGACGACCTTACTATTAATTTATGATCTGCTTTGACACCTGTTACAGCTCG 3157
2091 CAGCATTAGTAGTGACTTCAACATTTGGAATCCAAATGACAGATCTATGACCAAG 2147
3158 CAGCATTAGTAGTGACTTCAACATTTGGAATCCAAATGACAGATCTATGACCAAG 3214

RESULT 2
AAH78338
AAH78338 standard; cDNA; 11475 BP.
AAH78338;
26-NOV-2001 (first entry)
Nucleotide sequence of a starch branching enzyme designated F2.
Wheat; starch branching enzyme; BE1b; SBE; transgenic plant;
starch biosynthetic pathway; amylopectin; F2; amylose; ss.
Aegilops tauschii.
MO200162934-A1.
30-AUG-2001.
21-FEB-2001; 2001MO-AU000175.
21-FEB-2000; 2000AU-00005742.
(GSIR) COMMONWEALTH SCI & IND RES ORG.
(GOOD-) GOODMAN FIELDER LTD.
(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
Morell M, Rahman S;
WPI; 2001-570635/64.
Nucleic acids encoding wheat starch branching enzyme 1b, useful for
altering the amylose and amylopectin content of cereal plants, e.g. wheat
and barley.
Example 1; Fig 2; 103pp; English.
The present sequence encodes a wheat starch branching enzyme of Aegilops
tauschii, designated F2. A. tauschii is likely to be the ancestral D
genome donor of wheat. Probes isolated from the present sequence were
used to identify wheat II starch branching enzymes (SBEs) in wheat,
especially BE1b. The BE1b nucleic acids may be used to genetically
transform cereal plants such as wheat or barley and for altering their
nutritional content by modulating the starch biosynthetic pathway to vary
levels of amylopectin and/or amylose produced in the plant

Sequence 11475 BP; 3093 A; 2259 C; 2423 G; 3689 T; 0 U; 11 Other;
Query Match 98.9%; Score 2124; DB 5; Length 11475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2146; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

1 CGCGAGCTTCAACCCGCGCGACAGCTTGTCTCCCTTCATCGCTTCAATTAATA 60
1058 CGCGAGCTTCAACCCGCGCGACAGCTTGTCTCCCTTCATCGCTTCAATTAATA 1117
61 TCTCCATCACTCGAGTTCCGCGCTGCAATTCGCGCGGCGGTTGAGTGAATCTGGCGCA 120

1118 TCTCCATCACTCGAGTTCCGCGCTGCAATTCGCGCGGCGGTTGAGTGAATCTGGCGCA 1177
121 CTGGCTGACTCAATCACTACGCGGGGATGCGAGCTTCGCGGCTCCGCGCACTCG 180
1178 CTGGCTGACTCAATCACTACGCGGGGATGCGAGCTTCGCGGCTCCGCGCACTCG 1237
181 GTGTGGCGCGGCGCGGCGGTGAGTGGCGCGGCGGCTCGAGCGGAGGGCGGGCGG 240
1238 GTGTGGCGCGGCGCGGCGGTGAGTGGCGCGGCGGCTCGAGCGGAGGGCGGGCGG 1297
241 ACTTGGCGGTGCTGCTCTCTAGAGAAAGAACTCTCTGTAAGCGCTCTCTGTAAT 300
1298 ACTTGGCGGTGCTGCTCTCTAGAGAAAGAACTCTCTGTAAGCGCTCTCTGTAAT 1357
301 CTCCCGGCTGCTGCT 360
1358 CTCCCGGCTGCTGCT 1417
361 GCTGTTCCCAATTGATCTTCATGAGTGAAGAGATAGCTGATTTAGCGATTCGCGCTTC 420
1418 GCTGTTCCCAATTGATCTTCATGAGTGAAGAGATAGCTGATTTAGCGATTCGCGCTTC 1477
421 CTGAACCTGATTTTTCCTCCCGCGGGGAAATGGTTAGTCAACCGCGGCTGCTGTT 480
1478 CTGAACCTGATTTTTCCTCCCGCGGGGAAATGGTTAGTCAACCGCGGCTGCTGTT 1537
481 ACCAGGCTTGAATCAATCTCTGTTCAATCTGATATATATTTCTCATTTCTTTCTTC 540
1538 ACCAGGCTTGAATCAATCTCTGTTCAATCTGATATATATTTCTCATTTCTTTCTTC 1597
541 CTGTTCTGCTGTAATCAATCTCTGTTCAATCTGATATATATTTCTCATTTCTTTCTTC 600
1598 CTGTTCTGCTGTAATCAATCTCTGTTCAATCTGATATATATTTCTCATTTCTTTCTTC 1657
601 TTGCAAGCGCGGCTCTGAGCGCGCGGCTCTCCAGGGAAGTCTGCTGCGCGCGG 660
1658 TTGCAAGCGCGGCTCTGAGCGCGCGGCTCTCCAGGGAAGTCTGCTGCGCGCGG 1717
661 AGAG-GACGACTGGGCAAGTCCGCGCGCACTGTAAGATTCAGGTACACACACTGATG 719
1718 AGAGGCAAGCTTGGCAAGTCCGCGCGCACTGTAAGATTCAGGTACACACACTGATG 1777
720 CGGTAAATCTTCAATCAATGATTTTCACTTACCAATTCGCGGATGAACCAACCAACG 779
1778 CGGTAAATCTTCAATCAATGATTTTCACTTACCAATTCGCGGATGAACCAACCAACG 1837
780 TGGCTGAGGTTTGAAGCTTCTTCTATAGCATTTGAGTACTGCACTGCTGTTCAAT 839
1838 TGGCTGAGGTTTGAAGCTTCTTCTATAGCATTTGAGTACTGCACTGCTGTTCAAT 1897
840 TTGTTAGCCTTGGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
1898 TTGTTAGCCTTGGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1957
900 TCTAGCAAGACTTCAACATATATGACCGCTTTGCGGTTTCTGCTGCTGCTGCTGCT 959
1958 TCTAGCAAGACTTCAACATATATGACCGCTTTGCGGTTTCTGCTGCTGCTGCTGCT 2017
960 TGTATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1019
2018 TGTATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2077
1020 TGACAGGCGGAGCTGACAGAAATCTTCAATCTTCAAGACGACTGAGGCAATTTGAGAA 1079
2078 TGACAGGCGGAGCTGACAGAAATCTTCAATCTTCAAGACGACTGAGGCAATTTGAGAA 2137
1080 CAATCACTGATGTTTACCAAGAGATTAAGAACTTGTGTTGGGAGAAACCGCGAG 1139
2138 CAATCACTGATGTTTACCAAGAGATTAAGAACTTGTGTTGGGAGAAACCGCGAG 2197
1140 TTGTCCCAAAACAGAGAGATGGGCAAGAAATATCGAGATTGACCCAACTGAAGAAAT 1199
2198 TTGTCCCAAAACAGAGAGATGGGCAAGAAATATCGAGATTGACCCAACTGAAGAAAT 2257

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QY 1200 TTGGAGCCATCTTGACTACCGGTAAATCCCTACCCCGCTTGCTCATTTTGAATTA 1259
DB 2258 TTCCGGAGCCATCTTGACTACCGGTAAATCCCTACCCCGCTTGCTCATTTTGAATTA 2317
QY 1260 GGTCCCTTCATCATGCAAAATTTGGGGAACATCAAAAGAGACAAAGACTAGGACCACTT 1319
DB 2318 GGTCCCTTCATCATGCAAAATTTGGGGAACATCAAAAGAGACAAAGACTAGGACCACTT 2377
QY 1320 TCATACAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1379
DB 2378 TCATACAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2437
QY 1380 ACAATTTGCTCAAAATTTGCAATTAAGTAATCTCTCCGATCATTAATTAAGAGTGG 1439
DB 2438 ACAATTTGCTCAAAATTTGCAATTAAGTAATCTCTCCGATCATTAATTAAGAGTGG 2497
QY 1440 CAAACTGATGAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1499
DB 2498 CAAACTGATGAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2557
QY 1500 ATTCTAGAGGGGGGAAATCTACCACTTGGGAACTTAAGTTCTTAATCTTGGCCCTTTT 1559
DB 2558 ATTCTAGAGGGGGGAAATCTACCACTTGGGAACTTAAGTTCTTAATCTTGGCCCTTTT 2617
QY 1560 GTTTTGGGGGAAACACTTGTCTAAATTCGAATGATTTTGGGTATACCTCGGTGATTCGA 1619
DB 2618 GTTTTGGGGGAAACACTTGTCTAAATTCGAATGATTTTGGGTATACCTCGGTGATTCGA 2677
QY 1620 CAGATACAGCGAATACAAAGAAATTCGTCGCTATTGACCAACATGAAAGTGTGATGGA 1679
DB 2678 CAGATACAGCGAATACAAAGAAATTCGTCGCTATTGACCAACATGAAAGTGTGATGGA 2737
QY 1680 AGCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1739
DB 2738 AGCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2797
QY 1740 TATTATGAAACGCTCCACTGATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 1799
DB 2798 TATTATGAAACGCTCCACTGATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 2857
QY 1800 TTTTCCCTCTCTTTTCCAGTCTGAGGATGCTAATGCTAATGCTAATGCTAATGCTAAT 1859
DB 2858 TTTTCCCTCTCTTTTCCAGTCTGAGGATGCTAATGCTAATGCTAATGCTAATGCTAAT 2917
QY 1860 ATTATATCTCTGCTTTTCCCTATTTTCCAGTCTGAGGATGCTAATGCTAATGCTAAT 1919
DB 2918 ATTATATCTCTGCTTTTCCCTATTTTCCAGTCTGAGGATGCTAATGCTAATGCTAAT 2977
QY 1920 CTCCCTGAGGAGATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 1979
DB 2978 CT-CTGAGGAGATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 3036
QY 1980 GTTATATGCTACATTAACCACTAGCTTACGACTTACCAATTAAGTCTAATGCTAAT 2039
DB 3037 GTTATATGCTACATTAACCACTAGCTTACGACTTACCAATTAAGTCTAATGCTAAT 3096
QY 2040 GACCAAGTTACTATAAATTAATGATGCTGCTTTGCAACCTGTTAAGTCTGAGCACT 2099
DB 3097 GACCAAGTTACTATAAATTAATGATGCTGCTTTGCAACCTGTTAAGTCTGAGCACT 3156
QY 2100 TAGGTGACTTCAAAATTTGGAATCCAAATGAGATGATGATGAGCAAG 2147
DB 3157 TAGGTGACTTCAAAATTTGGAATCCAAATGAGATGATGATGAGCAAG 3204

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DE XX Nucleotide sequence of wheat starch branching enzyme 9 (BE1a).
XX XX wheat, starch branching enzyme; BE1a; BE1b; SBE; transgenic plant;
XX XX starch biosynthetic pathway; amylopectin; amylose; ss.
XX OS Triticum sp.
XX PN WO200162934-A1.
XX PD 30-AUG-2001.
XX PF 21-FEB-2001; 2001WO-AU000175.
XX PR 21-FEB-2000; 2000AU-00005742.
XX PA (CSTR) COMMONWEALTH SCI & IND RES ORG.
XX PA (GOOD-) GOODMAN FIELDER LTD.
XX PA (LIMA-) GRP LIMARAIN PACIFIC PTY LTD.
XX PI Morell M, Rahman S;
XX DR WPI, 2001-570635/64.
XX PT Nucleic acids encoding wheat starch branching enzyme 1b, useful for
XX PT altering the amylose and amylopectin content of cereal plants, e.g. wheat
XX PT and barley.
XX PS Example 1, Fig 1, 103bp; English.
XX CC The present sequence encodes wheat starch branching enzyme 9, designated
XX CC BE1a. The specification describes BE1b. BE1b is a type II starch
XX CC branching enzyme (SBE). The BE1b nucleic acids may be used to
XX CC genetically transform cereal plants such as wheat or barley and for
XX CC altering their nutritional content by modulating the starch biosynthetic
XX CC pathway to vary levels of amylopectin and/or amylose produced in the
XX CC plant
XX SQ Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 U; 0 Other;

Query Match 10.9%; Score 235; DB 5; Length 2726;
Best Local Similarity 96.0%; Pred. No. 2, 5e-55;
Matches 241; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 978 AGATACCTGAGAGATACGAGGAGCAACGCGAGGAGTGAATGATGACAGGGGAGCTGACG 1037
DB 200 AGATACCTGAGAGATACGAGGAGCAACGCGAGGAGTGAATGATGACAGGGGAGCTGACG 259
QY 1038 AGAACTTCATCTTCAGAACCGACTCAAGGCAATGTGGAACCAATCACTGATGCTTAA 1097
DB 260 AAAAATTGATCTTCAGAACCGACTCAAGGCAATGTGGAACCAATCACTGATGCTTAA 319
QY 1098 CCAAGAGTTTAAAGAACTAGTGTGGGGGAGAAACCGCAAGTTGTCGCAAAACAGAG 1157
DB 320 CCAAGAGTTTAAAGAACTAGTGTGGGGGAGAAACCGCAAGTTGTCGCAAAACAGAG 379
QY 1158 ATGGGCGAGAAATATACGAGATGACCCAACTGAAAGATTTTGGAGCCATCTTGAAT 1217
DB 380 ATGGGCGAGAAATATACGAGATGACCCAACTGAAAGATTTTGGAGCCATCTTGAAT 439
QY 1218 ACCGGTAAATGC 1228
DB 440 ACCGATACAGC 450

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RESULT 3
 AAH78337
 ID AAH78337 standard; cDNA, 2726 BP.
 XX
 AC AAH78337;
 XX
 DT 26-NOV-2001 (first entry)

RESULT 4
 AAH78351
 ID AAH78351 standard; DNA; 226 BP.
 XX
 AC AAH78351;
 XX
 DT 26-NOV-2001 (first entry)

DE	Nucleotide sequence of intron 5 fragment from D genome of wheat.
KX	Wheat; starch branching enzyme; BE1b; SBE; transgenic plant;
KM	starch biosynthetic pathway; amylopectin; amylose; ss.
XX	
CS	Triticum sp.
XN	MO200162934-A1.
PN	
PD	30-AUG-2001.
XX	
PF	21-FEB-2001; 2001WO-AU000175.
PR	21-FEB-2000; 2000AU-00005742.
KX	(CSIR) COMMONWEALTH SCI & IND RES ORG.
KX	(GOOD-) GOODMAN FIELDER LTD.
PA	(LIMA-) GRP LIMABRAIN PACIFIC PTY LTD.
KX	
P1	Morell M, Rahman S;
DR	WPI; 2001-570635/64.
XX	
PT	Nucleic acids encoding wheat starch branching enzyme Iib, useful for
PT	altering the amylose and amylopectin content of cereal plants, e.g. wheat
KT	and barley.
XX	
PS	Disclosure; Fig 4; 103pp; English.
CC	AH78351-54 represent intron 5 fragments from wheat. The specification
CC	describes a wheat starch branching enzyme, designated BE1b. BE1b is a
CC	type II search branching enzyme (SBE). The BE1b nucleic acids may be
CC	used to genetically transform cereal plants such as wheat or barley and
CC	for altering their nutritional content by modulating the starch
CC	biosynthetic pathway to vary levels of amylopectin and/or amylose
CC	produced in the plant
KX	
3Q	Sequence 226 BP; 64 A; 49 C; 40 G; 73 T; 0 U; 0 Other:
	Query Match 8.3%; Score 177.6; DB 5; Length 226;
	Best Local Similarity 91.4%; Pred. No. 1,1e-39;
	Matches 212; Conservative 0; Mismatches 14; Indels 6; Gaps 2;
2y	1901 ATCACTTACCGAGATGGGCTCCCTCGAGCGCAGTGTTAATGTTTCCTTAAGTCTCTTAACG 1960
Dc	1 ATCACTTACCGAGATGGGCT CCTGAGCGCATGTATGTCTTTAAAGCTT-----AAC 54
2y	1961 AGACACCTTCCAATTATTGTTAATNGTCACACTATTCACCACTAGCTTACGGACTTACA 2020
Dc	55 AGACACCTTCCAATTATTGTTAATNGTCACACTATTCACCACTAGCTTACGGACTTACA 114
2y	2021 AATTAGCTTAGCAATCTAGCACCACTTACTATAATTTATGATCTGGCTTTGCACCCTG 2080
Dc	115 AATTAGCTTAGCAATCTAGCACCACTTACTATAATTTATGATCTGGCTTTGCACCCTG 174
2y	2081 TTACAGCTGCGACATTAGTAGTGACTCTCAACAATTGGAAATCACAATGACG 2132
Dc	175 TTACAGCTGCGACATTAGTAGTGACTCTCAACAATTGGAAATCACAATGACG 226
RESULT 5	
ID	AH78353
KX	AH78353 standard; DNA; 217 BP.
KX	
3C	AH78353;
KX	
JT	26-NOV-2001 (first entry)
KX	
JE	Nucleotide sequence of intron 5 fragment from B genome of wheat.
KX	Wheat; starch branching enzyme; BE1b; SBE; transgenic plant;
KM	starch biosynthetic pathway; amylopectin; amylose; ss.
XX	

OS	Triticum sp.
XX	
PN	MO200162934-AI.
XX	
PD	30-AUG-2001.
XX	
PF	21-FEB-2001; 2001WO-AU000175.
XX	
PR	21-FEB-2000; 2000AU-00005742.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PA	(GOOD-) GOODMAN FIELDER LTD.
PA	(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
PI	Morell M, Rahman S;
XX	
DR	WPI; 2001-570635/64.
XX	
PT	Nucleic acids encoding wheat starch branching enzyme Iib, useful for
PT	altering the amylose and amylopectin content of cereal plants, e.g. wheat
PT	and barley.
PS	
XX	Disclosure; Fig 4; 103bp; English.
CC	AAT8351-54 represent intron 5 fragments from wheat. The specification
CC	describes a wheat starch branching enzyme, designated BElib. BElib is a
CC	type II starch branching enzyme (SBE). The BElib nucleic acids may be
CC	used to genetically transform cereal plants such as wheat or barley and
CC	for altering their nutritional content by modulating the starch
CC	biosynthetic pathway to vary levels of amylopectin and/or amylose
CC	produced in the plant
XX	
SQ	Sequence 217 BP; 63 A; 47 C; 39 G; 68 T; 0 U; 0 Other;
XX	
Query Match	7.6%; Score 164.2; DB 5; Length 217;
Best Local Similarity	95.5%; Pred.No. 6.7e-36;
Matches 169; Conservative	0; Mismatches 8; Indels 0; Gaps 0;
OY	1956 TAAGGAGCACCCTTCCAATTATGTGAATGGTCACCTATGCACCACTAGCTACTGGAC 2015
DB	41 TTAAACAGCACCTCTCATTTATTATTGTATAGTGTAAGTCACTATGCCAAGCTTACTGGAC 100
OY	2016 TTACAATTAGCTTAGCGAATAGTACACCACTTACTATAATTATGATCTGGCTTTGCA 2075
DB	101 TTCAAATATAGCTTAGCGAATAGTACACCACTTACTATAATTATGATCTGGCTTTGGA 160
OY	2076 CCTGTATACAGCTGACAGCATTTAGAGGTGACTTCAACATTTGGAATCCAAATGCAG 2132
DB	161 TCCTGTATACAGCTGACAGCATTTAGAGGTGACTTCAACATTTGGAATCCAAATGCAG 217
RESULT 6	
AAH78352	
ID	AAH78352 standard; DNA; 228 BP.
XX	
AC	AAH78352;
XX	
DT	26-NOV-2001 (first entry)
XX	
DE	Nucleotide sequence of intron 5 fragment from A genome of wheat.
XX	
KM	Wheat; starch branching enzyme; BElib; SBE; transgenic plant;
XX	starch biosynthetic pathway; amylopectin; amylose; ss.
OS	
XX	Triticum sp.
PN	MO200162934-AI.
PD	30-AUG-2001.
XX	
PF	21-FEB-2001; 2001WO-AU000175.
XX	
PR	21-FEB-2000; 2000AU-00005742.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (GOOD-) GOODMAN FIELDER LTD.
 PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
 XX Morell M, Rahman S;
 XX WPI; 2001-570635/64.
 XX Nucleic acids encoding wheat starch branching enzyme IIP, useful for
 PT altering the amylose and amylopectin content of cereal plants, e.g. wheat
 PT and barley.
 XX Disclosure; Fig 4; 103pp; English.
 XX AAH78351-54 represent intron 5 fragments from wheat. The specification
 CC describes a wheat starch branching enzyme, designated BRIB. BRIB is a
 CC type II starch branching enzyme (SBE). The BRIB nucleic acids may be
 CC used to genetically transform cereal plants such as wheat or barley and
 CC for altering their nutritional content by modulating the starch
 CC biosynthetic pathway to vary levels of amylopectin and/or amylose
 CC produced in the plant

XX Sequence 228 BP; 63 A; 53 C; 40 G; 72 T; 0 U; 0 Other;

Query Match 7.4%; Score 159.2; DB 5; Length 228;
 Best Local Similarity 88.9%; Pred. No. 1.8e-34;

Matches 208; Conservative 0; Mismatches 18; Indels 8; Gaps 3;

QY 1901 ATCACTTACCGAGATGGGCTCCCTGAGCCGATGTATGTTCTTTAACTTCCCTTAAG 1960
 Db 1 ATCACTTACCGAGATGGGCT--CTGAGCCGATGTATGTTCTTTAACTT---AAC 54
 QY 1961 AGACACCTTCCAAATTTATGTTAATGCT--CACTATCCACCACTAGCTTACTGACCTTA 2018
 Db 55 AGACACCTTCCAAATTTATGTTAATGCTAATTTACCACTAGCTTACTGACCTTA 114
 QY 2019 CAAATTAGCTTACTGATGATGACCACTTACTATTAATTTATGATCTGGCTTTTGACCC 2078
 Db 115 CAACTTAGCTTACTGATGATGACCACTTACTATTAATTTATGATCTGGCTTTTGACATCC 174
 QY 2079 TGTTCAGCTGCGACGATTTAGTGTGACTTAACTTGAATGCAATGACG 2132
 Db 175 TGTTCAGCTGCGACGATTTAGTGTGACTTCAACATTTGAATGCAATGACG 228

RESULT 7
 ID AAV05639 standard; cDNA to mRNA; 3015 BP.

XX AAV05639;

XX 25-MAR-2003 (revised)
 DT 01-MAY-1998 (first entry)

XX Rice type IV starch branching enzyme cDNA.

XX Rice; type IV starch branching enzyme; amylopectin synthesis; ds.

XX Oryza sativa.

XX Key Location/Qualifiers
 FH CDS 129..2654
 FT /*tag= a
 FT sig_peptide 129..287
 FT /*tag= b
 FT mat_peptide 288..2651
 FT /*tag= c
 FT /product= "type_IV_starch_branching_enzyme"

XX JP10004970-A.
 XX 13-JAN-1998.
 PD

XX 24-JUN-1996; 96JP-00162983.
 XX 24-JUN-1996; 96JP-00162983.
 XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
 PA (MITK) MITSUI TOATSU CHEM INC.
 XX WPI; 1998-133625/13.
 DR P-PBDB; AAM41763.
 XX Rice starch branching enzyme gene - synthesises amylopectin to yield high
 PT quality starch.
 XX Claim 4; Page 5-8; 13pp; Japanese.
 XX The present sequence encodes the rice type IV starch branching enzyme,
 CC which has the ability to synthesise amylopectin. The quality of starch is
 CC improved by the use of the protein. (Updated on 25-MAR-2003 to correct PA
 CC field.)

XX Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 U; 0 Other;

Query Match 6.3%; Score 135.8; DB 2; Length 3015;
 Best Local Similarity 76.3%; Pred. No. 3.4e-27;

Matches 167; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1006 GGCGGAGTGAACATGACAGGGGGGAGCTGACAGAACTTCAATCTTCAGAACCGACTCA 1065
 Db 449 GGCGGAGTGAACATGAGTTGTGCTGAGCAAACTTGAATCTTCAGAAAGTGAATCA 508
 QY 1066 GGCGATTGTGGAAACATGACATGATGTGTAAACCAAGATTAGGAATGCTGCGG 1125
 Db 509 AGACATTTGAGGAAATGTGCTGAGGTGTATCATAAGATGATGATGACCACTGCGA 568
 QY 1126 GGAGAAACCGGAGTTGTCCCAAAACCGAGAGTGGGAGAAATATPACGATTGACCC 1185
 Db 569 GGATTAACCGAGTTATGCCACACGAGAGATGGGAGAAATATPACGAAATTGACCC 628
 QY 1186 AACCTGAAAGATTTTGGAGCCATCTTGACTACCGGTA 1224
 Db 629 AATGCTGAAAGATTTGGAACCATCTTGACTACCGGTA 667

RESULT 8
 ID ADA71289 standard; DNA; 2655 BP.

XX ADA71289;

XX 20-NOV-2003 (first entry)

XX Rice gene, SEQ ID 4612.

XX Plant; bacterial infection; fungal infection; viral infection; rice;
 KW gene; ds.

XX Oryza sativa.

XX WO2003000898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Qian S, Tao Y, Whittham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.

DR

XX Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PI bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.

XX Claim 6, SEQ ID NO 4612; 899bp; English.

XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.

XX Sequence 2655 BP; 714 A; 529 C; 680 G; 732 T; 0 U; 0 Other;

XX Query Match 5.5%; Score 117.8; DB 7; Length 2655;
 Best Local Similarity 67.1%; Pred. No. 4e-22;
 Matches 167; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

XX 978 AGATACCTGAAGATATGAGAGAGCAACCGCGGAAAGTGAACATGACAGGGGACTGCAG 1037
 Db AGATACCTGAAGATATGAGAGAGCAACCGTTTGAAGAGAGAGAGATTCACAGATG 328

XX 1038 AGAACTTCATCTTCGAAACCGACTCAGGATGTGGAACATCATCTGATGTGTA 1097
 Db GCAGAGCAAGCATTAAGAAAGTGAAGATGAGAGAGAGAGATGAGGTGTA 388

XX 1098 CCAAGAGATTAAAGAACTGATCGTGGGGAGAAACCGGAGTTTCCCAAAACAGAGAG 1157
 Db TCAGAGATGCTGATGAGAACCACTGTGAGAGATTAACAGAGATTTCACACACAGAGAG 448

XX 1158 ATGGGCAAGAAATATATGAGATTGACCAACACCTGAAGATTTTGGAGCCATCTTGACT 1217
 Db ATGGGCAAGAAATATATGCAAAATGACCAATGCTGGAAGATTGGGAACCATCTTGACT 508

XX 1218 ACCGCTAAT 1226
 Db 509 ACCGCAAT 517

XX RESULT 9
 AD08218 standard; DNA; 2304 BP.

XX AD08218;
 DT 18-DEC-2003 (first entry)

XX Rice DNA sequence Seq ID523 related to grain filling.

XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KM carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KM tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KM wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KM gene; ds; plant.

XX Oryza sativa.
 XX WO200300905-A2.

XX 03-JAN-2003.
 XX 21-JUN-2002; 2002WO-1B002450.

XX 22-JUN-2001; 2001US-0300112P.
 XX 26-SEP-2001; 2001US-0325277P.
 XX 20-DEC-2001; 2001US-0342327P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Zhu T, Cheng W, Briggs S, Cooper B, Golf SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Riecke D;
 XX

XX WPI; 2003-229341/22.
 DR P-PsDB; AD08219.

XX New plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 PT in the plant grain useful in generating plants having improved
 PT nutritional properties.

XX Claim 35; SEQ ID NO 523; 130bp; English.

XX This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is a
 CC DNA sequence encoding a rice protein of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/publshedpct_sequences.

XX Sequence 2304 BP; 610 A; 457 C; 620 G; 617 T; 0 U; 0 Other;

XX Query Match 5.4%; Score 116; DB 9; Length 2304;
 Best Local Similarity 67.2%; Pred. No. 1.2e-21;
 Matches 164; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

XX 978 AGATACCTGAAGATATGAGAGAGCAACCGCGGAAAGTGAACATGACAGGGGACTGCAG 1037
 Db AGATACCTGAAGATATGAGAGAGCAACCGTTTGAAGAGAGAGAGATTCACAGATG 346

XX 1038 AGAACTTCATCTTCGAAACCGACTCAGGATGTGGAACATCATCTGATGTGTA 1097
 Db GCAGAGCAAGCATTAAGAAAGTGAATCAAGACATGAGAAATGTGACTAGGGGTGTA 406

XX 1098 CCAAGAGATTAAAGAACTGATCGTGGGGAGAAACCGGAGTTTCCCAAAACAGAGAG 1157
 Db 407 TCAGAGATGCTGATGAGAACCACTGTGAGAGATTAACCAAGATTAATCCACACAGAGAG 466

XX 1158 ATGGGCAAGAAATATATGAGATTGACCAACACCTGAAGATTTTGGAGCCATCTTGACT 1217
 Db ATGGGCAAGAAATATATGCAAAATGACCAATGCTGGAAGATTGGGAACCATCTTGACT 526

XX 1218 ACCG 1221
 Db 527 ACCG 530

XX RESULT 10
 AAH78342 standard; cDNA; 2968 BP.

XX AAH78342;
 XX 26-NOV-2001 (first entry)

XX Nucleotide sequence of wheat starch branching enzyme (BEIIb).
 DE wheat; starch branching enzyme; BEIIb; SBE; transgenic plant;
 KM starch biosynthetic pathway; amylopectin; amylose; ss.

XX Triticum sp.

PN WO200162934-A1.
XX 30-AUG-2001.
XX 21-FEB-2001, 2001MO-AU000175.
XX 21-FEB-2000, 2000AU-00005742.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX (GOOD-) GOODMAN FIELDER LTD.
XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX Morell M, Rahman S;
XX WPI, 2001-570635/64.
XX Nucleic acids encoding wheat starch branching enzyme IIb, useful for
XX altering the amylose and amylopectin content of cereal plants, e.g. wheat
XX and barley.
XX Claim 6, Fig 9, 103pp; English.
XX The present sequence encodes a wheat starch branching enzyme, designated
XX BB1b. BB1b is a type II starch branching enzyme (SBE). The BB1b
XX nucleic acids may be used to genetically transform cereal plants such as
XX wheat or barley and for altering their nutritional content by modulating
XX the starch biosynthetic pathway to vary levels of amylopectin and/or
XX amylose produced in the plant
XX Sequence 2968 BP; 784 A; 626 C; 796 G; 756 T; 0 U; 6 Other;
SQ
XX Query Match 3.9%; Score 84.4; DB 5; Length 2968;
XX Best Local Similarity 61.3%; Pred. No. 1.3e-12;
XX Matches 136; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 1010 GAAGTGAACATGACAGGGGGAGCTGCAGAGAACTTCAATCTTCCAGAACCCGACTCAGGCG 1069
DB 497 GAACCAAGCCTACAGATGAGAGGTGAAGATAGTATTTGCTTCCAGAGCAAAATCAGGTT 556
QY 1070 ATTGTGAAACATCATCTGATGCTGTATACCAAGAGATTAGAGATGCTGGGGGAG 1129
DB 557 AGTGAAGAAATGATGCTGAAGACACGACAGAAATGACAAAGATCACTACGAGGAG 616
QY 1130 AAACCGGAGTGTCCCAAAACAGAGATGGGCAAAATATAGAGATTGACCCACACA 1189
DB 617 AAATTACGCAATTCGCCACACCGGAAATGACAGAAATATACGAGATTGACCCACAG 676
QY 1190 CTGAAGATTTTCGAGCCATCTTACTACCGGTAATGCTTA 1231
DB 677 CTCGAGACTTTAAGTACCATCTTGTAGTATGATATAGCCTA 718
RESULT 11
ABK15494
ID ABK15494 standard, cDNA; 3039 BP.
XX AC ABK15494;
XX 08-MAY-2002 (first entry)
XX Wheat starch branching enzyme IIb cDNA from clone wdk2c_pk009.j17.
XX Wheat starch branching enzyme; starch synthesis; transgenic plant;
XX wdk2c_pk009.j17; antibody; gene mapping; expressed sequence tag; EST;
XX gene; ss.
XX Triticum aestivum.
XX OS
XX FH Key Location/Qualifiers
XX FT CDS 3..2570
XX FT /*tag=a
XX FT /product="starch branching enzyme IIb"
XX FT /partial

PT /note="No start codon shown. The sequence from
FT nucleotides 481-3039 is specifically claimed in claim 3
FT of the specification and is shown as Seq ID. 1"
XX US2002002713-A1.
XX 03-JAN-2002.
XX 23-FEB-2001, 2001US-00792127.
XX 01-MAR-2000, 2000US-0186098P.
XX (ALLE) ALLEN S M.
XX (BECK) BECKLES D M.
XX (BUTL) BUTLER K H.
XX (PEAR) PEARLSTEIN R W.
XX Allen SM, Beckles DM, Butler KH, Pearlstein RW,
XX WPI, 2002-178959/23.
XX P-PSDB; AAU76219.
XX Novel isolated polypeptide having starch IIB enzyme activity, useful for
XX preparing antibodies to the proteins which are used to detect the
XX polypeptides in situ in cells or in vitro in cell extracts.
XX Claim 3, Page 17-18; 27pp; English.
XX This invention relates to the cDNA and protein sequences of a novel wheat
XX starch branching enzyme IIB enzyme. Starch branching enzymes are
XX responsible for the formation of alpha 1-6 linkages in amylopectin in the
XX starch synthesis pathway. The nucleotide sequence of the invention is
XX useful for producing a transgenic plant expressing the starch branching
XX enzyme. The protein sequence is useful for preparing antibodies against
XX starch branching enzyme IIB protein, which are useful for detecting the
XX proteins in situ in cells, or in vitro in cell extracts. The protein is
XX also useful for selecting an isolated polynucleotide that affects the
XX level of expression of a starch branching enzyme IIB protein or enzyme
XX activity in a plant cell. All or substantial portion of the nucleotide
XX sequence can be used as probe for genetic and physical mapping of the
XX information in a plant breeding in order to develop lines with
XX desired phenotypes. A polynucleotide fragment is useful for isolating
XX cDNAs and genes encoding homologous proteins from the same or other plant
XX species. They are also useful as DNA hybridisation probes or as
XX polymerase chain reaction (PCR) amplification primers. The fragments are
XX also useful for creating transgenic plants and may be useful as
XX restriction fragment length polymorphism markers. Nucleic acid probes
XX derived from the cDNA sequence may also be used for physical mapping or
XX for fluorescence in situ hybridisation (FISH) mapping. The present
XX sequence represents the wheat starch branching enzyme IIB cDNA from clone
XX wdk2c_pk009.j17
SQ Sequence 3039 BP; 836 A; 624 C; 783 G; 796 T; 0 U; 0 Other;
XX Query Match 3.9%; Score 84.4; DB 6; Length 3039;
XX Best Local Similarity 61.3%; Pred. No. 1.3e-12;
XX Matches 136; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 1010 GAAGTGAACATGACAGGGGGAGCTGCAGAGAACTTCAATCTTCCAGAACCCGACTCAGGCG 1069
DB 372 GAACCAAGCCTACAGATGAGAGGTGAAGATAGTATTTGCTTCCAGAGCAAAATCAGGTT 431
QY 1070 ATTGTGAAACATCATCTGATGCTGTATACCAAGAGATTAGAGATGCTGGGGGAG 1129
DB 432 AGTGAAGAAATGATGCTGAAGACACGACGAGAAATGACAAAGATCACTACGAGGAG 491
QY 1130 AAACCGGAGTGTCCCAAAACAGAGATGGGCAAAATATAGAGATTGACCCACACA 1189
DB 492 AAATTACGCAATTCGCCACACCGGAAATGACAGCAAAATATACGAGATTGACCCACAG 551
QY 1190 CTGAAGATTTTCGAGCCATCTTACTACCGGTAATGCTTA 1231

Db 552 CTCGAGACTTTAAGTACCATCTTGATGATGATATAGCCTA 593

RESULT 12

AAH78341 ID AAH78341 standard; DNA, 3962 BP.

XX AC AAH78341;

XX DT 26-NOV-2001 (first entry)

XX DE Partial sequence of a starch branching enzyme designated F2.

XX KM Wheat; starch branching enzyme; BE11b; SBE; transgenic plant;
XX KM starch biosynthetic pathway; amylopectin; F2; amylose; ss.

XX CS Aegilops tauschii.

XX PN WO200162934-A1.

XX PD 30-AUG-2001.

XX PF 21-FEB-2001; 2001WO-AU000175.

XX PR 21-FEB-2000; 2000AU-00005742.

XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX PA (GOOD-) GOODMAN FIELDER LTD.

XX PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

XX PI Morell M, Rahman S;

XX DR WPI; 2001-570635/64.

XX PT Nucleic acids encoding wheat starch branching enzyme IIb, useful for
XX PT altering the amylose and amylopectin content of cereal plants, e.g. wheat
XX PT and barley.

XX PS Claim 6; Fig 8; 103pp; English.

XX CC The present sequence represents a partial genomic sequence of a wheat
XX CC starch branching enzyme of Aegilops tauschii, designated F2. A. tauschii
XX CC is likely to be the ancestral D genome donor of wheat. Probes isolated F2
XX CC were used to identify type II starch branching enzymes (SBEs) in wheat,
XX CC especially BE11b. The BE11b nucleic acids may be used to genetically
XX CC transform cereal plants such as wheat or barley and for altering their
XX CC nutritional content by modulating the starch biosynthetic pathway to vary
XX CC levels of amylopectin and/or amylose produced in the plant

XX SQ Sequence 3962 BP; 1091 A; 778 C; 809 G; 1284 T; 0 U; 0 Other;

Query Match 3.8%; Score 82.2; DB 5; Length 3962;

Best Local Similarity 61.4%; Pred. No. 6.2e-12; Mismatches 83; Indels 0; Gaps 0;

Matches 132; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

2Y 1010 GAAGTGAACATGACAGGGGGAAGTCTGAGAGAACTTCAATCTTCAGAACGACTCAGGGC 1069

Db 1156 GAAACAGGCTACAGATGAGGTGAAGATGATTTGGCTTCAGAGACAAATCAGGTT 1215

2Y 1070 ATTGTGAAACATCACTGATGCTGAACCAAGAGATTAGGAATCTAGTCGCGGGGAG 1129

Db 1216 AGTGAAGAAATGATGCTGTAAGACAGAGCAAGATGACAAAGATCATCTACAGAGGAG 1275

2Y 1130 AAACCGCGAGTGTCCCAAAACAGAGAGAGGCGCAAAATATACGATGACCCACACA 1189

Db 1276 AAATTAAGCAATCTGCGACACCGGAAATGACAGCAAAATATACGATTGACCCACAG 1335

2Y 1190 CTGAAGATTTTCGAGGCACTTGTGACTACCGGTA 1224

Db 1336 CTCGAGACTTTAAGTACCATCTTGATGATGATATAGCCTA 1370

RESULT 13

AAH78343 ID AAH78343 standard; DNA, 8381 BP.

XX AC AAH78343;

XX DT 26-NOV-2001 (first entry)

XX DE Partial genomic sequence of wheat starch branching enzyme (BE11b).

XX KM Wheat; starch branching enzyme; BE11b; SBE; transgenic plant;

XX KM starch biosynthetic pathway; amylopectin; amylose; ss.

XX OS Triticum sp.

XX PN WO200162934-A1.

XX PD 30-AUG-2001.

XX PF 21-FEB-2001; 2001WO-AU000175.

XX PR 21-FEB-2000; 2000AU-00005742.

XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX PA (GOOD-) GOODMAN FIELDER LTD.

XX PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

XX PI Morell M, Rahman S;

XX DR WPI; 2001-570635/64.

XX PT Nucleic acids encoding wheat starch branching enzyme IIb, useful for
XX PT altering the amylose and amylopectin content of cereal plants, e.g. wheat
XX PT and barley.

XX PS Claim 6; Page 95-98; 103pp; English.

XX CC The present sequence represents a partial genomic sequence of a wheat
XX CC starch branching enzyme, designated BE11b. BE11b is a type II starch
XX CC branching enzyme (SBE). The BE11b nucleic acids may be used to
XX CC genetically transform cereal plants such as wheat or barley and for
XX CC altering their nutritional content by modulating the starch biosynthetic
XX CC pathway to vary levels of amylopectin and/or amylose produced in the
XX CC plant

XX SQ Sequence 8381 BP; 2134 A; 1788 C; 1829 G; 2608 T; 0 U; 22 Other;

Query Match 3.8%; Score 82.2; DB 5; Length 8381;

Best Local Similarity 61.4%; Pred. No. 9.5e-12; Mismatches 83; Indels 0; Gaps 0;

Matches 132; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1010 GAAGTGAACATGACAGGGGGAAGTCTGAGAGAACTTCAATCTTCAGAACGACTCAGGGC 1069

Db 1616 GAAACAGGCTACAGATGAGGTGAAGATGATTTGGCTTCAGAGACAAATCAGGTT 1675

QY 1070 ATTGTGAAACATCACTGATGCTGAACCAAGAGATTAGGAATCTAGTCGCGGGGAG 1129

Db 1676 AGTGAAGAAATGATGCTGTAAGACAGAGCAAGATGACAAAGATCATCTACAGAGGAG 1735

QY 1130 AAACCGCGAGTGTCCCAAAACAGAGAGAGGCGCAAAATATACGATGACCCACACA 1189

Db 1736 AAATTAAGCAATCTGCGACACCGGAAATGACAGCAAAATATACGATTGACCCACAG 1795

QY 1190 CTGAAGATTTTCGAGGCACTTGTGACTACCGGTA 1224

Db 1796 CTCGAGACTTTAAGTACCATCTTGATGATGATATAGCCTA 1830

RESULT 14

AAO73750 ID AAO73750 standard; cDNA to mRNA; 2919 BP.

XX AC AAO73750;

RESULT 13

DT 05-JUL-1995 (first entry)
 XX Rice starch branching enzyme.
 DE Sarch branching enzyme; rice; starch content; ds.
 XX
 XX Oryza sativa.
 OS
 XX
 XX Key Location/Qualifiers
 FT 5/UTR 1..127
 FT /tag= a
 FT transit_peptide 128..322
 FT /tag= b
 FT mat_peptide 323..2606
 FT /tag= c
 FT /product= "branching_enzyme"
 FT 2603..2919
 FT 3/UTR /tag= d
 FT
 XX JF06261767-A.
 XX
 XX 20-SEP-1994.
 XX
 XX 22-OCT-1993; 93JP-00265171.
 XX
 XX 29-OCT-1992; 92JP-00291719.
 XX
 XX (MITSU) GYOSAI SHOKUBUTSU BIO KENKYUSHO.
 XX WPI: 1994-337418/42.
 XX P-PSDB; AAR60811.
 DR
 XX New gene of branching enzyme of rice starch - useful for increasing
 PT starch yield of grain.
 PS
 PS Claim 1; Page 9-12; 13pp; Japanese.
 XX
 XX The rice starch branching enzyme is encoded by the cDNA sequence
 CC AA073750. The starch content of rice grains can be increased by
 CC increasing the expression of branching enzyme in rice plants
 XX
 SQ Sequence 2919 BP; 755 A; 590 C; 800 G; 774 T; 0 U; 0 Other;
 Query Match 3.7%; Score 79.4; DB 2; Length 2919;
 Best Local Similarity 63.2%; Pred. No. 3.2e-11;
 Matches 122; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
 QY 1039 GAAATTCATCTTGAAGACGACCTCAGGCGCATTTGGAACAATCACTGATGCTGAAC 1098
 DB 436 GAGAGTTGAGAGCTGAAGTTGAGATTGATCATCTGAGCAAGACGTTGAGAGCGCTGAA 495
 QY 1099 CAAAGAGATTAAAGACTAGTCGTGGGGAGAAACCGCAGTTGTCACAAAACAGAGAG 1158
 DB 496 GAGAGTGTGTAAGATTAGCTGCTGAGAGAAACACAGAGTTGTCACACAGAGAG 555
 QY 1159 TGGGCAAAATATACAGATTGACCCCAACTGAAAGATTTTGGAGGCATTTGACTA 1218
 DB 556 TGGGCAAAATATATCCAGATGACCTATGCTTAATGCTAATAGTACCATCTTGAAAT 615
 QY 1219 CCGGTAATGCCCTA 1231
 DB 616 TCGATATAGCCTA 628
 RESULT 15
 ADC07807
 ID ADC07807 standard; DNA; 2307 BP.
 XX
 XX ADC07807;
 XX
 XX 18-DEC-2003 (first entry)
 XX
 XX Rice DNA sequence seq ID73 related to grain filling.

XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarcane;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW Gene; ds; plant.
 XX
 XX Oryza sativa.
 OS
 XX
 XX WO2003000905-A2.
 XX
 XX 03-JAN-2003.
 XX
 XX 21-JUN-2002; 2002MO-IB002450.
 XX
 XX 22-JUN-2001; 2001US-0300112P.
 XX 26-SEP-2001; 2001US-0325277P.
 XX 20-DEC-2001; 2001US-0342327P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Kategiri F, Kreps J, Provart N, Riecke D;
 XX
 XX WPI: 2003-229341/22.
 XX P-PSDB; ADC07808.
 DR
 XX
 XX New plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 PT in the plant grain useful in generating plants having improved
 PT nutritional properties.
 XX
 PS Claim 2; SEQ ID NO 73; 130pp; English.
 XX
 XX This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarcane, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is a
 CC DNA sequence encoding a rice protein of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/publishepct_sequences.
 XX
 SQ Sequence 2307 BP; 608 A; 465 C; 620 G; 614 T; 0 U; 0 Other;
 Query Match 3.7%; Score 78.6; DB 5; Length 2307;
 Best Local Similarity 90.5%; Pred. No. 4.7e-11;
 Matches 95; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
 QY 1618 AACGATACACCGGATACAGAGAAATTCGTCGTATATGA-CCAACTGAAGTGTGATT 1676
 DB 364 ACCGGAATACGATGATACAGAGAAATTCGTCGTATATGA-CCAACTGAAGTGTGATT 423
 QY 1677 GGAAGCATTTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721
 DB 424 GGAATCATTTTCTCGTGTATGAAAAGCTTGATTACCCGAG 468
 Search completed: April 10, 2004, 04:00:00
 Job time : 846.046 secs

Mon Apr 12 10:24:23 2004

us-09-508-377-10_copy_1058_3204.rml

Page 1

GenCore version 5.1.6
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CM nucleic - nucleic search, using SW model

Run on: April 10, 2004, 03:15:35 ; Search time 152.665 Seconds
(without alignments)
7804.525 Million cell updates/sec

Title: US-09-508-377-10_COPY_1058_3204
Sequence: 1 cgcacgtccaccccccgc.....tgcagatactatgcacagag 2147

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	243	11.3	2853	4	US-09-609-040-3
2	90.8	4.2	2446	4	US-09-731-166-9
3	68.8	3.2	7218	1	US-08-232-463-14
4	61.6	2.9	2720	4	US-09-731-166-11
5	58.4	2.7	2087	4	US-09-257-894-9
6	58.4	2.7	2165	4	US-09-257-894-8
7	58.4	2.7	2665	4	US-09-257-894-1
8	58.4	2.7	2725	3	US-08-941-445A-14
9	58.2	2.7	3074	3	US-09-087-877-1
10	58.2	2.7	3074	4	US-09-658-499-1
11	53.8	2.5	507	4	US-09-257-894-5
12	45	2.1	7218	1	US-08-232-463-14
13	43.4	2.0	879	4	US-09-621-876-2813
14	42.2	2.0	279	4	US-09-913-294A-3795
15	41.2	1.9	364	4	US-09-621-876-17202
16	41	1.9	819	4	US-09-252-991A-7968
17	41	1.9	3657	4	US-09-252-991A-8028
18	41	1.9	3661	4	US-09-252-991A-8018
19	40.2	1.9	832	1	US-09-621-876-2813
20	40	1.9	1427	4	US-07-994-133-1
21	40	1.9	1427	6	5196304-1
22	39.6	1.8	3001	4	US-09-539-333D-184
23	38.4	1.8	1281	3	US-09-105-537-19
24	38.4	1.8	13613	3	US-09-105-537-3
25	38.4	1.8	38506	4	US-09-320-878-19
26	38.4	1.8	38506	4	US-09-421-908-1
27	38.4	1.8	38506	4	US-09-657-440-19

28	37.6	1.8	330	4	US-09-313-294A-7061	Sequence 7061, Ap
29	37.6	1.8	395	4	US-09-894-844-45	Sequence 45, Appl
30	37.6	1.8	1600	4	US-09-434-288-10	Sequence 10, Appl
31	37.6	1.8	4252	2	US-08-475-844-4	Sequence 4, Appl
32	37.6	1.8	4252	5	PCT-US95-08429-4	Sequence 4, Appl
33	37.2	1.7	2830	1	US-07-882-292-1	Sequence 1, Appl
34	37.2	1.7	2830	2	US-08-331-644-1	Sequence 1, Appl
35	37.2	1.7	2830	5	PCT-US93-04102-1	Sequence 1, Appl
36	37.2	1.7	1664976	4	US-08-916-421B-1	Sequence 1, Appl
37	36.8	1.7	4403765	3	US-09-103-840A-2	Sequence 2, Appl
38	36.8	1.7	4411529	3	US-09-103-840A-2	Sequence 1, Appl
39	36.6	1.7	441	4	US-09-252-991A-16329	Sequence 16329, A
40	36.6	1.7	1029	4	US-09-252-991A-16157	Sequence 16157, A
41	36.6	1.7	1272	4	US-09-894-844-47	Sequence 16045, A
42	36.6	1.7	1296	4	US-09-894-844-47	Sequence 47, Appl
43	36.6	1.7	1980	4	US-09-252-991A-16555	Sequence 16555, A
44	36.6	1.7	2561	4	US-09-616-289-48	Sequence 48, Appl
45	36.6	1.7	12732	3	US-09-060-756-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-609-040-3
Sequence 3, Application US/09609040
Patent No. 6570066
GENERAL INFORMATION:
APPLICANT: Wilmittzer, et al.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE
TITLE OF INVENTION: CONCENTRATION AND COMPOSITION IN PLANTS
FILE REFERENCE: 514413-3515.1
CURRENT APPLICATION NUMBER: US/09/609,040
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: PCT/EP92/00302
PRIOR FILING DATE: 1992-02-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 2853
TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: CDS
LOCATION: (313)..(2499)
OTHER INFORMATION: BRANCHING ENZYME
US-09-609-040-3

Query Match	11.3%	Score 243;	DB 4;	Length 2853;
Best Local Similarity	98.0%	Pred. No. 1.8e-60;		
Matches 246;	Conservative	0;	Mismatches 5;	Indels 0;
Gaps	0;			
QY	978	AGATACCTGAAGATTCGAGGCAACGCGGAAGTGAACATGACAGGGGACTGCAG	1037	
DB	272	AGATACCTGAAGATTCGAGGCAACGCGGAAGTGAACATGACAGGGGACTGCAG	331	
QY	1038	AGAACTTCAATCTTCGAGACCGACTCAGGGCTGTGTGAAACATCACTGATGGTGTAA	1097	
DB	332	AAAACTTCAATCTTCGAGACCGACTCAGGGCTGTGTGAAACATCACTGATGGTGTAA	391	
QY	1098	CCAAAGGCTTAAGAACTAGTCGTGGGGGAGAAACCGGAGTGTCCCAACAGAG	1157	
DB	392	CCAAAGGCTTAAGAACTAGTCGTGGGGGAGAAACCGGAGTGTCCCAACAGAG	451	
QY	1158	ATGGGCAAAAATATACGAGATTGACCCAACTGAGAGATTTTCGAGCCATCTTGACT	1217	
DB	452	ATGGGCAAAAATATACGAGATTGACCCAACTGAGAGATTTTCGAGCCATCTTGACT	511	
QY	1218	ACCGGTAATGC 1228		
DB	512	ACCGGTAATGC 522		

```
RESULT 2
US-09-731-166-9
; Sequence 9, Application US/09731166
; Patent No. 6639126
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent J. H.
; APPLICANT: Singletary, George W.
; TITLE OF INVENTION: Production of Modified Polysaccharides
; FILE REFERENCE: 35718/206348
; CURRENT APPLICATION NUMBER: US/09/731.166
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/169,993
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2446
; TYPE: DNA
; ORGANISM: Zea mays
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: SBE11a
; OTHER INFORMATION: Genbank Accession No. 6639126 U65948
; NAME/KEY: CDS
; LOCATION: (2)...(2446)
US-09-731-166-9

Query Match
Best Local Similarity 4.2%; Score 90.8; DB 4; Length 2446;
Matches 116; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1067 GGCATTGTGGAACATCTAGTGTGTAACCAAGAGTTAGGAAGTCTGCTGGG 1126
DB 293 GGTACTGTGTGGAACCAAAATGATGTGTGAGCATCAAAAGCCACTCTGTGAG 352
QY 1127 GAGAAACCGGAGTGTGTCACCAACGAGATGGGAGAAATATACAGATTGACCA 1186
DB 353 GAGAAACCGGAGTGTGTCACCAACGAGATGGGAGAAATATACAGATTGACCA 412
QY 1187 AACTGGAAGATTTTCGAGGCACTTGTACTACCGGTA 1224
DB 413 ATGTTGGAAGGTTTCGGGGTCACTTGACTACGATA 450

RESULT 3
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEFFLINGER, F.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
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; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

Query Match
Best Local Similarity 3.2%; Score 68.8; DB 1; Length 7218;
Matches 19; Conservative 234; Mismatches 151; Indels 0; Gaps 0;

QY 219 TCGAGCGGAGGCGCGGCGGAGCTTGCCGTCGCTGCTCTCAGAAAGAGCTCT 278
DB 1032 TCGAGCTTGCGTCGAGGTCGAGGAGCTTGCGATYYYYYYYYYYYYYYYY 1091
QY 279 CGTACCCCTGCTCTCTCAATCTCCCGCTGCTTGCTGCTCCCTGCTCTCT 338
DB 1092 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1151
QY 339 GGGCGGCGATGGCGCTGTGATGCTGTCCCATGATCTCATGATGAGAGATAG 398
DB 1152 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1211
QY 399 CTGATAGGCGATTCGCTCTCTGAACTGTAATTTTCCCGCGGGAATGCGTTA 458
DB 1212 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1271
QY 459 GTCTACCCAGGCGCTGCTGTACACAGGCTTGATCATTCCTGTTCAATGATATA 518
DB 1272 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1331
QY 519 TATTTCTCATCTTTTCTCTGCTGCTGCTGTAAGTGTGCGCTTTTCA 578
DB 1332 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1391
QY 579 CTATGTAGTATCTTGTGATTTGACGGCGGCTGAGCGG 622
DB 1392 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1435

RESULT 4
US-09-731-166-11
; Sequence 11, Application US/09731166
; Patent No. 6639126
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent J. H.
; APPLICANT: Singletary, George W.
; TITLE OF INVENTION: Production of Modified Polysaccharides
; FILE REFERENCE: 35718/206348
; CURRENT APPLICATION NUMBER: US/09/731.166
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/169,993
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2720
; TYPE: DNA
; ORGANISM: Zea mays
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: SBE1B
OTHER INFORMATION: Genbank Accession No. 6639126 AF072725
NAME/KEY: CDS
LOCATION: (101)...(2500)
US-09-731-166-11

Query Match
Best Local Similarity 76.0%; Pred. No. 1.9e-07;
Matches 76; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1622 GATACAGCGAATACAGAGAAATTCGTCCTATTGACCAACATGAAGGTGATTGGAAG 1681
DB 513 GGACAGCCCTCTATAGAGAAATCCGTTCAACATTGATGACATGAAGAGAGGCTTGGAAG 572
QY 1682 CATTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721
DB 573 CCTTCTCCGTAATGAGAACTTTGATTATCCGAG 612

RESULT 5
US-09-257-894-9
Sequence 9, Application US/09257894
Patent No. 6376749

GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749e1 Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-257-894-9

Query Match
Best Local Similarity 74.0%; Pred. No. 1.4e-06;
Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1622 GATACAGCGAATACAGAGAAATTCGTCCTATTGACCAACATGAAGGTGATTGGAAG 1681
DB 413 GGACAGCCCTCTATAGAGAAATCCGTTCAACATTGATGACATGAAGAGGCTTGGAAG 472
QY 1682 CATTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721
DB 473 CCTTCTCCGTAATGAGAACTTTGATTATCCGAG 512

RESULT 6
US-09-257-894-8/c
Sequence 8, Application US/09257894
Patent No. 6376749

GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749e1 Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-257-894-8

Query Match
Best Local Similarity 74.0%; Pred. No. 1.4e-06;
Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1622 GATACAGCGAATACAGAGAAATTCGTCCTATTGACCAACATGAAGGTGATTGGAAG 1681
DB 1675 GGACAGCCCTCTATAGAGAAATCCGTTCAACATTGATGACATGAAGAGGCTTGGAAG 1616
QY 1682 CATTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721
DB 1615 CCTTCTCCGTAATGAGAACTTTGATTATCCGAG 1576

RESULT 7
US-09-257-894-1

Sequence 1, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Brogile, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 79..2476
US-09-257-894-1

Query Match 2.7%; Score 58.4; DB 4; Length 2665;
Best Local Similarity 74.0%; Pred. No. 1.6e-06;
Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
DB 1622 GATACAGCAATACAGAGAAATTCGCTGCTATTGACCAACATGAAGGTGATTGGAAG 1661
491 GGTACAGCCTCTATAGAGATCCGTTCAACATGATGATGAACATGAAGAGGCTTGAAG 550
QY 1682 CATTTCTCGTGTATGAAAAGCTTGATTTACCCGCGAG 1721
DB 551 CCTTCCCGTAGTATGAGAACTTTGATTATGCGCAG 590
RESULT 9
US-08-941-445A-14
Sequence 14, Application US/08941445A
GENERAL INFORMATION:
PATENT NO. 6107060
APPLICANT: Keeling, Peter
APPLICANT: Guan, Haining
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Circle
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2725 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: mRNA
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Zea mays
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 91..264
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 265..2487
FEATURE:
NAME/KEY: CDS
LOCATION: 91..2490
US-08-941-445A-14

Query Match 2.7%; Score 58.4; DB 3; Length 2725;
Best Local Similarity 74.0%; Pred. No. 1.6e-06;
Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
DB 1622 GATACAGCAATACAGAGAAATTCGCTGCTATTGACCAACATGAAGGTGATTGGAAG 1661
503 GGTACAGCCTCTATAGAGATCCGTTCAACATGATGATGAACATGAAGAGGCTTGAAG 562
QY 1682 CATTTCTCGTGTATGAAAAGCTTGATTTACCCGCGAG 1721
DB 563 CCTTCCCGTAGTATGAGAACTTTGATTATGCGCAG 602
RESULT 9
US-09-087-277-1
Sequence 1, Application US/09087277B
GENERAL INFORMATION:
PATENT NO. 6169226
APPLICANT: EK, Bo
APPLICANT: KHOSWOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakar
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558

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EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism:beli gene
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
OTHER INFORMATION: (potato)
FEATURE:
NAME/KEY: CDS
LOCATION: (189)..(2825)
FEATURE:
NAME/KEY: sig peptide
LOCATION: (189)..(332)
FEATURE:
NAME/KEY: mat peptide
LOCATION: (333)..(2825)
FEATURE:
NAME/KEY: misc feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
OTHER INFORMATION: n wherein n = A, C, G or T.
FEATURE:
NAME/KEY: misc feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
OTHER INFORMATION: or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Thr.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1895)..(1898)
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
OTHER INFORMATION: or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-087-277-1

Query Match      2.7%; Score 58.2; DB 3; Length 3074;
Best Local Similarity 72.8%; Pred. No. 2e-06;
Matches 75; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1619 ACAGATACAGCGAATACAAAGAAATTCGTCTGCTATTGACCAACATGAAGTGGATTGG 1678
DB 775 ACAGGATTCACAGTACAAAGAACTGAGGAGGCAATTGACAAATATGAGGTTGGTGG 834

QY 1679 AAGCATTTTCGTGTTATGAAAAGCTTGATTACCCGAG 1721
DB 835 AAGCTTTTCGTGTTATGAAAAGCTTGATTACCTCGTAG 877

RESULT 10
US-09-658-499-1
Sequence 1, Application US/09568499
Patent No. 6469231
GENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamshid

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APPLICANT: LARSSON, Claes-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/658,499
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/087,277
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR FILING DATE: 1996-11-28
PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9601506-0
PRIOR FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism:beli gene
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
OTHER INFORMATION: (potato)
NAME/KEY: CDS
LOCATION: (189)..(2825)
NAME/KEY: sig peptide
LOCATION: (189)..(332)
NAME/KEY: mat peptide
LOCATION: (333)..(2825)
NAME/KEY: misc feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
OTHER INFORMATION: n wherein n = A, C, G or T.
NAME/KEY: misc feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
OTHER INFORMATION: or Phe.
NAME/KEY: misc feature
LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
NAME/KEY: misc feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
NAME/KEY: misc feature
LOCATION: (1895)..(1898)
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
OTHER INFORMATION: or Phe.
NAME/KEY: misc feature
LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-658-499-1

Query Match      2.7%; Score 58.2; DB 4; Length 3074;
Best Local Similarity 72.8%; Pred. No. 2e-06;
Matches 75; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1619 ACAGATACAGCGAATACAAAGAAATTCGTCTGCTATTGACCAACATGAAGTGGATTGG 1678
DB 775 ACAGGATTCACAGTACAAAGAACTGAGGAGGCAATTGACAAATATGAGGTTGGTGG 834

QY 1679 AAGCATTTTCGTGTTATGAAAAGCTTGATTACCCGAG 1721
DB 835 AAGCTTTTCGTGTTATGAAAAGCTTGATTACCTCGTAG 877

RESULT 11
US-09-257-894-5/c
Sequence 5, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Brogille, Karen E.

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APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749e1 Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
CLASSIFICATION:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-257-894-5
Query Match
Best Local Similarity 69.5%; Pred. No. 1.2e-05;
Matches 73; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1126 GGAGAAACCGGAGTGTCCCAAAACCGAGATGGGCGAATAATACGAGATTGACCC 1185
DB 112 GAACGAGTTGAGTGTCCCAAAACCGAGATGGGCGAATAATACGAGATTGACCC 53
QY 1186 AACACTGAAAGATTTCGAGGCCATCTTGACTACCGGTATGCTT 1230
DB 52 CATGTTGCAAGGTATAGTACATCTTGAGTATCGGTACAGCTT 8
RESULT 12
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEFFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMTU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 893149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ19pt-Fls
US-08-232-463-14
Query Match
Best Local Similarity 2.1%; Score 45; DB 1; Length 7218;
Matches 6; Conservative 145; Mismatches 80; Indels 0; Gaps 0;
QY 967 TTTCGTGTGATGATCTGAGATATCGAGAGCAACCGCGAGTGAACATGACAG 1026
DB 1442 TTTCGTACRR 1383
QY 1027 GGGGACTGCAGAACTTCACTTCAGAACCGACTCAGGCTTGTGAAACAATAC 1086
DB 1382 RRR 1323
QY 1087 TGATGTGTAACCAAGAGTTAAGACTGAGGAGGAGAAACCGAGTGTCTCC 1146
DB 1322 RRR 1263
QY 1147 AAAACGAGATGGGCGAATAATATGAGATTGACCCAACTGAAAGA 1197
DB 1262 RRR 1212
RESULT 13
US-09-621-976-2813
Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J. B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J. Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 235..399


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QY 121 CTGGCTGACTCAATCACTACGCGGGGATGCGAGCTTCGCGGTGTCGGCGCGGACTCTCG 180
Db 1278 CTGGCTGACTCAATCACTACGCGGGGATGCGAGCTTCGCGGTGTCGGCGCGGACTCTCG 1237
QY 181 GTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 1238 GTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1297
QY 241 ACTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 1298 ACTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1357
QY 301 CTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 1358 CTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1417
QY 361 GCTGTTCCCGCAATTCATCTCCATGATGAGAGAGTACTGATTAAGCGATCGCGCTTC 420
Db 1418 GCTGTTCCCGCAATTCATCTCCATGATGAGAGAGTACTGATTAAGCGATCGCGCTTC 1477
QY 421 CTGAACCTGATATTTTTCCTCCCGCGCGGAAATGCTTAGTGCACCCAGCGCTGTGT 480
Db 1478 CTGAACCTGATATTTTTCCTCCCGCGCGGAAATGCTTAGTGCACCCAGCGCTGTGT 1537
QY 481 ACCAGCGCTTGATCATCTTCGTTTCAATTCGATATATATTTTCTCATTTCTTTCTTC 540
Db 1538 ACCAGCGCTTGATCATCTTCGTTTCAATTCGATATATATTTTCTCATTTCTTTCTTC 1597
QY 541 CTGTTCTGCTGTAATCTGCAATGTTGGGCTTTTTCATATGATGATCACTTCGAT 600
Db 1598 CTGTTCTGCTGTAATCTGCAATGTTGGGCTTTTTCATATGATGATCACTTCGAT 1657
QY 601 TTGAGCGCGCGCGCTCGTGAAGCGCGCGCGCTTCGAGGAGAGTCTGTCGCTGAAGCG 660
Db 1658 TTGAGCGCGCGCGCTCGTGAAGCGCGCGCGCTTCGAGGAGAGTCTGTCGCTGAAGCG 1717
QY 661 AGAG-GAGGACTTGGCAAGTCCGCGCGCACTGAGAAATTAAGTAAACACACCTGTCG 719
Db 1718 AGAGGAGGACTTGGCAAGTCCGCGCGCACTGAGAAATTAAGTAAACACACCTGTCG 1777
QY 720 CGGTAATCTTCATACATCGTATTCATCTTACCAATGCGGATGAGAAACCAACGCGA 779
Db 1778 CGGTAATCTTCATACATCGTATTCATCTTACCAATGCGGATGAGAAACCAACGCGA 1837
QY 780 TGGCGTGAAGTTTCGAGCTTTCTTATCAAGCATTTGCAATCTGCACTGCTTGTTCAT 839
Db 1838 TGGCGTGAAGTTTCGAGCTTTCTTATCAAGCATTTGCAATCTGCACTGCTTGTTCAT 1897
QY 840 TTGTTAGCTTGGCGCGCGCGCTGCTGTCGCGCGCACTGAGAAATTAAGTAAATGAT 899
Db 1898 TTGTTAGCTTGGCGCGCGCGCTGCTGTCGCGCGCACTGAGAAATTAAGTAAATGAT 1957
QY 900 TCTAGCAAGAACTTCACAAATATATGACCGTTTGGGTTTCTGATGCTGCTTACAT 959
Db 1958 TCTAGCAAGAACTTCACAAATATATGACCGTTTGGGTTTCTGATGCTGCTTACAT 2017
QY 960 TGTATATTTTGTGCTGTATGATCTGAAAGATTAAGAGAGCAACGCGGAGAGTAA 1019
Db 2018 TGTATATTTTGTGCTGTATGATCTGAAAGATTAAGAGAGCAACGCGGAGAGTAA 2077
QY 1020 TGAACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1079
Db 2078 TGAACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2137
QY 1080 CAATCACTGATGCTGTAACCAAGAGTTAAAGAACTGATGCTGGGCGAGAAACCGCGAG 1139
Db 2138 CAATCACTGATGCTGTAACCAAGAGTTAAAGAACTGATGCTGGGCGAGAAACCGCGAG 2197
QY 1140 TTGTCCCAAAACAGAGATGCGCGAGAAATTAAGAGTTGACCAACATGAAAGAT 1199
Db 2198 TTGTCCCAAAACAGAGATGCGCGAGAAATTAAGAGTTGACCAACATGAAAGAT 2257
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QY 1200 TTGGAGCCATCTTACTACCGGTAATGCTTACCGCGCTTGTGCTCATTTTGAATTA 1259
Db 2258 TTGGAGCCATCTTACTACCGGTAATGCTTACCGCGCTTGTGCTCATTTTGAATTA 2317
QY 1260 GGTCTTTTCAATCAGCAATTTTGGGGAACATCAAAAGACAAAGACTAGGACCACT 1319
Db 2318 GGTCTTTTCAATCAGCAATTTTGGGGAACATCAAAAGACAAAGACTAGGACCACT 2377
QY 1320 TCATACAGATCCCTTCGTGCTGAGATTAAGTAAATGATTAATGATGCT 1379
Db 2378 TCATACAGATCCCTTCGTGCTGAGATTAAGTAAATGATTAATGATGCT 2437
QY 1380 ACAATTTGCTCAAAATTTGCAATCGAATACGTCTCCGATCATTAATTAAGAGTG 1439
Db 2438 ACAATTTGCTCAAAATTTGCAATCGAATACGTCTCCGATCATTAATTAAGAGTG 2497
QY 1440 CAACCTGATGAAATGTTGCTGAGATGCTTATGATTTTACTTGTGTAATTCCTCA 1499
Db 2498 CAACCTGATGAAATGTTGCTGAGATGCTTATGATTTTACTTGTGTAATTCCTCA 2557
QY 1500 ATTCTAGGCGGGAATCTACCAATGAGGAACTAGTTCTTATCTTGTGCGCTTTT 1559
Db 2558 ATTCTAGGCGGGAATCTACCAATGAGGAACTAGTTCTTATCTTGTGCGCTTTT 2617
QY 1560 GTTTTGGGGAACACATTCGTAATTTGAAATGATTTTGGTATACCTGCTGATTC 1619
Db 2618 GTTTTGGGGAACACATTCGTAATTTGAAATGATTTTGGTATACCTGCTGATTC 2677
QY 1620 CAGATACGCGAATACAAAGAAATTCGCTGCTATTAAGCAACAGAGAGTGA 1679
Db 2678 CAGATACGCGAATACAAAGAAATTCGCTGCTATTAAGCAACAGAGAGTGA 2737
QY 1680 AGCATTTTCTGCTGATTAAGAAAGCTTGAATTAACCGAGGTAATTTAAAGCTTAT 1739
Db 2738 AGCATTTTCTGCTGATTAAGAAAGCTTGAATTAACCGAGGTAATTTAAAGCTTAT 2797
QY 1740 TATATGAAAGCGCTCCGCTAGCTGTAATTTGATATCTTAAGAAATTTAAATTCG 1799
Db 2798 TATATGAAAGCGCTCCGCTAGCTGTAATTTGATATCTTAAGAAATTTAAATTCG 2857
QY 1800 TTTTCCCTCTCTTTTTCAGAGCTGAGGATCGTAAATGCGATCTTAAGAA 1859
Db 2858 TTTTCCCTCTCTTTTTCAGAGCTGAGGATCGTAAATGCGATCTTAAGAA 2917
QY 1860 ATTATATCTCTTTTTCCTTATTTTTCAGTGTGAAGGATCACTTAACGAGATGG 1919
Db 2918 ATTATATCTCTTTTTCCTTATTTTTCAGTGTGAAGGATCACTTAACGAGATGG 2977
QY 1920 CTCCTGAGCGCAATGATATGCTTTTAAGTCTTTAAGAGACACCTTCAATTAAT 1979
Db 2978 CTCCTGAGCGCAATGATATGCTTTTAAGTCTTTAAGAGACACCTTCAATTAAT 3037
QY 1980 GTTAATGTCATATTCACCAATAGTACTGACCTTAACAAATTAAGTACT 2039
Db 3038 GTTAATGTCATATTCACCAATAGTACTGACCTTAACAAATTAAGTACT 3097
QY 2040 GACCAATTAATTAATTAATGATGCTTGTGAACCTTACAGCTGAGAGATTA 2099
Db 3098 GACCAATTAATTAATTAATGATGCTTGTGAACCTTACAGCTGAGAGATTA 3157
QY 2100 TAGTGACTTCAACAAATGGAATCCAAATGAGATTAATGACAGAG 2147
Db 3158 TAGTGACTTCAACAAATGGAATCCAAATGAGATTAATGACAGAG 3205
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RESULT 2
US-10-434-893A-1
; Sequence 1, Application US/10434893A
; Publication No. US2004006083A1
; GENERAL INFORMATION:
; APPLICANT: Ahmed Regina
; APPLICANT: Matthew Kennedy Morell
; APPLICANT: Sadequr Rahman

1 TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and
2 FILE REFERENCE: 69425
3 CURRENT APPLICATION NUMBER: US/10/434,893A
4 CURRENT FILING DATE: 2003-05-09
5 NUMBER OF SEQ ID NOS: 11
6 SOFTWARE: PatentIn version 2.1
7 SEQ ID NO 1
8 LENGTH: 2554
9 TYPE: DNA
10 ORGANISM: Hordeum vulgare
11 FEATURE:
12 OTHER INFORMATION: SSBELIA CDNA
13 US-10-434-893A-1

Query Match 9.4%; Score 201.4; DB 12; Length 2554;
Best Local Similarity 93.0%; Pred. No. 3.6e-48;
Matches 211; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1002 AAACGGGGAAGTGAACATGACAGGGGGAAGTGAAGAACTTCACTTTCAGAACCGA 1061
DB 5 AGATGGCGGAAGTGAACATGACAGGGGGAAGTGAAGAACTTCACTTTCAGAACCGA 64
QY 1062 CTCAGGCACTTGTGAAGAACATCACTGATGTGAACCAAGAGTGAAGAACTTATGCG 1121
DB 65 CTCAGGCACTTGTGAAGAACATCACTGATGTGAACCAAGAGTGAAGAACTTATGCG 124
QY 1122 TGGGGGAGAAACCGGAGTGTGTCACAAACAGAGATGGGCGAAATATACGAGATTG 1181
DB 125 TGGGGGAGAAACCGGAGTGTGTCACAAACAGAGATGGGCGAAATATACGAGATTG 184
QY 1182 ACCCAACACTGAGAAAGATTTTCGAGCCACTTGTGACTCCGGTATGCG 1228
DB 185 ACCCAACACTGAGAAAGATTTTCGAGCCACTTGTGACTCCGGTATGCG 231

RESULT 3
US-10-434-893A-2
1 Sequence 2, Application US/10434893A
2 Publication No. US20040060083A1
3 GENERAL INFORMATION:
4 APPLICANT: Ahmed Regina
5 APPLICANT: Matthew Kennedy Morell
6 APPLICANT: Sadegur Rahman
7 TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and starch
8 FILE REFERENCE: 69425
9 CURRENT APPLICATION NUMBER: US/10/434,893A
10 CURRENT FILING DATE: 2003-05-09
11 NUMBER OF SEQ ID NOS: 11
12 SOFTWARE: PatentIn version 2.1
13 SEQ ID NO 2
14 LENGTH: 2780
15 TYPE: DNA
16 ORGANISM: Hordeum vulgare
17 FEATURE:
18 OTHER INFORMATION: SSBELIB CDNA
19 US-10-434-893A-2

Query Match 4.2%; Score 90.8; DB 12; Length 2780;
Best Local Similarity 63.1%; Pred. No. 2.9e-15;
Matches 140; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 1010 GAAGTGAACATGACAGGGGGAAGTGAAGAACTTCACTTTCAGAACCGACTCAGGCG 1069
DB 298 GAACCAAGCTGACAGATGAGAGTGAAGAACTTCACTTTCAGAACCGACTCAGGCT 357
QY 1070 ATTGTGAAGAACATCACTGATGTGAACCAAGAGTGAAGAACTTATGCGTGGGGGAG 1129
DB 358 ACTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 417
QY 1130 AAACCGGAGTGTGTCACAAACAGAGATGGGCGAAATATACGAGATTGACCCCAAC 1189

DB 418 AAATATGACATGTCGACACACCCGGAATGACAGCAATATACGACATTGACCCCAATG 477
QY 1190 CTGAAGATTTTCGAGACCACTTGTACTACCGGTATGCCCTA 1231
DB 478 CTCGAGACTTAAAGTACACTTGTAGTATGATGATGATGATGATGATGATGATGATG 519

RESULT 4
US-09-792-127-3
1 Sequence 3, Application US/09792127
2 Patent No. US20020002713A1
3 GENERAL INFORMATION:
4 APPLICANT: Allen, Steve
5 APPLICANT: Beckles, Diane M.
6 APPLICANT: Butler, Karla
7 APPLICANT: Pearlstein, Rich
8 TITLE OF INVENTION: Starch Branching Enzyme IIb
9 FILE REFERENCE: B81439 US NA
10 CURRENT APPLICATION NUMBER: US/09/792,127
11 CURRENT FILING DATE: 2001-02-23
12 PRIOR APPLICATION NUMBER: 60/186098
13 PRIOR FILING DATE: 2000-03-01
14 NUMBER OF SEQ ID NOS: 5
15 SOFTWARE: Microsoft Office 97
16 SEQ ID NO 3
17 LENGTH: 3039
18 TYPE: DNA
19 ORGANISM: Triticum aestivum
20 US-09-792-127-3

Query Match 3.9%; Score 84.4; DB 9; Length 3039;
Best Local Similarity 61.3%; Pred. No. 2.5e-13;
Matches 136; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 1010 GAAGTGAACATGACAGGGGGAAGTGAAGAACTTCACTTTCAGAACCGACTCAGGCG 1069
DB 372 GAACCAAGCTGACAGATGAGAGTGAAGAACTTGTGCTTCAGAACCAATACAGGTT 431
QY 1070 ATTGTGAAGAACATCACTGATGTGAACCAAGAGTGAAGAACTTATGCGTGGGGGAG 1129
DB 432 AGTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 491
QY 1130 AAACCGGAGTGTGTCACAAACAGAGATGGGCGAAATATACGAGATTGACCCCAAC 1189
DB 492 AAATATGACATGTCGACACACCCGGAATGACAGCAATATACGACATTGACCCCAAC 551
QY 1190 CTGAAGATTTTCGAGACCACTTGTACTACCGGTATGCCCTA 1231
DB 552 CTCGAGACTTAAAGTACACTTGTAGTATGATGATGATGATGATGATGATGATGATG 593

RESULT 5
US-10-434-893A-4
1 Sequence 4, Application US/10434893A
2 Publication No. US20040060083A1
3 GENERAL INFORMATION:
4 APPLICANT: Ahmed Regina
5 APPLICANT: Matthew Kennedy Morell
6 APPLICANT: Sadegur Rahman
7 TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and starch
8 FILE REFERENCE: 69425
9 CURRENT APPLICATION NUMBER: US/10/434,893A
10 CURRENT FILING DATE: 2003-05-09
11 NUMBER OF SEQ ID NOS: 11
12 SOFTWARE: PatentIn version 2.1
13 SEQ ID NO 4
14 LENGTH: 6550
15 TYPE: DNA
16 ORGANISM: Aegilops tauschii
17 FEATURE:
18 NAME/KEY: MISC FEATURE
19 LOCATION: (1)...(6550)

OTHER INFORMATION: n is a, c, g or t
FEATURE:
OTHER INFORMATION: partial SSBELIB gene
US-10-434-893A-4

Query Match 3.8%; Score 82.2; DB 12; Length 6550;
Best Local Similarity 61.4%; Pred. No. 2e-12;
Matches 132; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1010 GAAGTGAATGACAGAGGGGAGCTGCAGAGAACTTCACTTCCAGACGAGCTCAGGGC 1069
DB 1616 GAAACAGGCTCAGAGATGAGGTGAGATGATTTGCTTCAGACCAATCAGGTT 1675
QY 1070 ATTGTGAAACAATCACTGATGTTGTTACCAAGAGATTAGAGACTAGTGGGGAG 1129
DB 1676 AGTGAAGAAATTTGATGTTGAGACACGACGAGATGACAAAGATCATCTACAGAGGAG 1735
QY 1130 AAACCCGAGTTGTCCCAAAACAGAGATGGCGAGAAATATACGATTGACCCACA 1189
DB 1736 AATTAAGCATTTGCGACACACCGGAAATGACAGCAAAATATACGATTGACCCACA 1795
QY 1190 CTGAAGAATTTTGGAGCCACTTGTACTACCGTA 1224
DB 1796 CTCGAGACTTTAAGTACCACTTGTAGTATCGTA 1830

RESULT 6
US-09-792-127-1
Sequence 1, Application US/09792127
Patent No. US20020002713A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Beckles, Diane M.
APPLICANT: Butler, Karla
APPLICANT: Pearlstein, Rich
TITLE OF INVENTION: Starch Branching Enzyme IIb
FILE REFERENCE: B1439 US NA
CURRENT APPLICATION NUMBER: US/09/792,127
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/166098
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 2559
TYPE: DNA
ORGANISM: Triticum aestivum
US-09-792-127-1

Query Match 3.0%; Score 64.2; DB 9; Length 2559;
Best Local Similarity 74.3%; Pred. No. 2.2e-07;
Matches 81; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1123 GGGGAGAAACCGCGAGTTGTCCAAAACAGAGATGGGCGAGAAATATACGAGTTGA 1182
DB 5 GAGGAGAAATTAAGCATTTCTCCACACCGGAAATGACAGCAAAATATACGAGTTGA 64
QY 1183 CCCAACACTGAAGATTTTGGAGGCATTTTGAATACCGGTAAATGCTTA 1231
DB 65 CCCAACGCTCCGAGACTTTAAGTACCATCTTGAATATAGCTTA 113

RESULT 7
US-10-424-599-130848
Sequence 130848, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 130848
LENGTH: 470
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MBT3847_89163C.1
US-10-424-599-130848

Query Match 3.0%; Score 63.6; DB 12; Length 470;
Best Local Similarity 59.3%; Pred. No. 9.2e-08;
Matches 108; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 1548 TGTGGCTTTTGTGTTGGGGAACACATTCCTAATTCGATGATTTGGGTATACCT 1607
DB 154 TTTTGCACTTTTGATACCTACTATCTGTAATTTATACGTAAATTTTAAATGCTA 213
QY 1608 CGGTGATTTCAACAGATACGCGAATACAGAGAAATTCGTGCTGCTATGACCAATGA 1667
DB 214 TTTTAAATCAGATTAATGACAAATACAAAGATTGCGTTATGAATGACAAAGCTGA 273
QY 1668 AGGTGATTTGAGATTTTTCGTGTTATGAAAAGCTTGATTTACCCGAGTAAAT 1727
DB 274 AGCGGCTCGATTAATTTTCACTGTTATGAAAATTTGCTTCCACGCAAGTATTA 333
QY 1728 TT 1729
DB 334 TT 335

RESULT 8
US-09-938-842A-337
Sequence 337, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 337
LENGTH: 2577
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-337

Query Match 2.8%; Score 59.8; DB 9; Length 2577;
Best Local Similarity 73.8%; Pred. No. 4.5e-06;
Matches 76; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 1619 ACAGATACGCGATACAGAGAAATTCGTGCTATTTGACCAATGAGGTGATTCG 1678
DB 527 ACGATATGGCGACTATACAGAAATCTGCTGAAGAAATGAGAAATGAGGTGATTCG 586
QY 1679 AAGCATTTTCTGCTGTTATGAAAAGCTTGATTTACCCGAG 1721
DB 587 AGCATTTTCTGCTGTTATGAAAATTTGCTTCACTCGAAG 629

RESULT 9

US-09-938-842A-337
Sequence 337, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME AND METHODS OF USE
FILE REFERENCE: S001300-3 US/09/938,842A
CURRENT APPLICATION NUMBER: US/09-08-24
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 337
LENGTH: 2577
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-337

Query Match 2.8%; Score 59.8; DB 11; Length 2577;
Best Local Similarity 73.8%; Pred. No. 4.5e-06;

Matches 76; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1619 ACAGATACGCGAATCAAGAGATTGCTGCTATGACCAATGAAAGTGGATTGG 1678
DB 527 ACCGATATGGGAGTACAGAAACTGCGTGAAGAAATGACAGAAATGAAAGTGG 586

QY 1679 AAGCATTTCTCGTGGTTATGAAAAGCTTGATTTACCCGAG 1721
DB 587 AGCGATTTCTCGTGGTTATGAAAATTTGGCTTCACTGAG 629

RESULT 10

US-10-056-454A-18
Sequence 18, Application US/10056454A
Publication No. US20030166919A1

GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Unidema Blvd.
CITY: Newcastle

STATE: Delaware
COUNTRY: United States of America
ZIP: 19720

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 3231 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-056-454A-18

Query Match 2.8%; Score 59.8; DB 14; Length 3231;

Best Local Similarity 73.8%; Pred. No. 5.3e-06;
Matches 76; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1619 ACAGATACGCGAATCAAGAGATTGCTGCTATGACCAATGAAAGTGGATTGG 1678
DB 814 ACAGATATGGGAGTACAGAAACTGCGTGAAGAAATGACAGAAATGAAAGTGG 873

QY 1679 AAGCATTTCTCGTGGTTATGAAAAGCTTGATTTACCCGAG 1721
DB 874 AAGCTTTCTCGTGGTTATGAAAATTTGGCTTCACTGAG 916

RESULT 11

US-10-424-599-130849
Sequence 130849, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 130849

LENGTH: 5164
TYPE: DNA
ORGANISM: Glycine max

FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_89164C.1
US-10-424-599-130849

Query Match 2.7%; Score 58.8; DB 12; Length 5164;
Best Local Similarity 73.5%; Pred. No. 1.5e-05;

Matches 75; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1620 CAGATACGCGAATCAAGAGATTGCTGCTATGACCAATGAAAGTGGATTGGA 1679
DB 927 CCGTATGAGACATCAAGAAAGTGGTTATGAAAATGACAGCAAGAGCGGTTGGA 986

QY 1680 AAGCATTTCTCGTGGTTATGAAAAGCTTGATTTACCCGAG 1721
DB 987 TAGATTTCTCGTGGTTATGAAAATTTGGCTTCACTGAG 1028

RESULT 12

US-10-397-954A-1
Sequence 1, Application US/10397954A
Publication No. US2003022120A1

GENERAL INFORMATION:
APPLICANT: Pearlstein, Richard W.
APPLICANT: Broglie, Karen E.

APPLICANT: Hines, Christopher F.
TITLE OF INVENTION: Maize Starch Containing Elevated Amounts of Actual Amylose

FILE REFERENCE: BB1510 US NA
CURRENT APPLICATION NUMBER: US/10/397,954A
CURRENT FILING DATE: 2003-03-26

PRIOR APPLICATION NUMBER: 60/368,387
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 60/381,534
PRIOR FILING DATE: 2002-05-16

NUMBER OF SEQ ID NOS: 6
SOFTWARE: Microsoft Word 97
SEQ ID NO 1

LENGTH: 2443
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(2443)

OTHER INFORMATION: SBEII modified region
US-10-397-954A-1

Query Match 2.7%; Score 58.4; DB 15; Length 2443;
Best Local Similarity 74.0%; Pred. No. 1.1e-05;
Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1622 GATACAGCGAATACAGAGAAATTCGTCTATTGACCAACATGAGGTGATTGGAAG 1681
DB 418 GGTACAGCCCTCTATAGAAAGATCCGTTGACATTTGATGAAATGAGAGAGGCTTGGAAG 477

QY 1682 CATTTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721
DB 478 CCTTCTCCGATGATGAGAGATTGATTATATGCGAG 517

RESULT 13
US-10-397-954A-1/C
Sequence 1, Application US/10397954A
Publication No. US2003022120A1

GENERAL INFORMATION:
APPLICANT: Pearlstein, Richard W.
APPLICANT: Bregille, Karen E.
APPLICANT: Hines, Christopher F.
TITLE OF INVENTION: Maize Starch Containing Elevated Amounts of Actual Amylose
FILE REFERENCE: B81510 US NA
CURRENT APPLICATION NUMBER: US/10/397,954A
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: 60/368,387
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 60/381,534
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Microsoft Word 97
SEQ ID NO 1
LENGTH: 2443
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(2443)
OTHER INFORMATION: SBEII modified region
US-10-397-954A-1

Query Match 2.7%; Score 58.4; DB 15; Length 2443;
Best Local Similarity 74.0%; Pred. No. 1.1e-05;

Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1622 GATACAGCGAATACAGAGAAATTCGTCTATTGACCAACATGAGGTGATTGGAAG 1681
DB 2024 GGTACAGCCCTCTATAGAAAGATCCGTTGACATTTGATGAAATGAGAGAGGCTTGGAAG 1965

QY 1682 CATTTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721
DB 1964 CCTTCTCCGATGATGAGAGATTGATTATATGCGAG 1925

RESULT 14
US-10-056-454A-17
Sequence 17, Application US/10056454A
Publication No. US20030166919A1

GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Uniquest Blvd.
CITY: Newcast
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-056-454A-17

Query Match 2.7%; Score 58.2; DB 14; Length 2529;
Best Local Similarity 72.8%; Pred. No. 1.3e-05;
Matches 75; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1619 ACAGATACAGCGAATACAGAGAAATTCGTCTATTGACCAACATGAAAGGTGATTGG 1678
DB 501 ACAGGATTCACAGTACAGAAACTAGAGGAGCAATTGACAGTATGAGGAGGTTGG 560

QY 1679 AAGCATTTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721
DB 561 AAGCTTTTCTCGTGTATGAAAAGGTTTCACTCGTAG 603

RESULT 15
US-10-056-454A-16
Sequence 16, Application US/10056454A
Publication No. US20030166919A1

GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Uniquest Blvd.
CITY: Newcast
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-056-454A-16

Query Match 2.7%; Score 58.2; DB 14; Length 2576;
Best Local Similarity 72.8%; Pred. No. 1.3e-05;
Matches 75; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1619 ACAGATACAGCGAATACAGAGAAATTCGTCTATTGACCAACATGAAAGGTGATTGG 1678
DB 508 ACAGGATTCACAGTACAGAAACTAGAGGAGCAATTGACAGTATGAGGAGGTTGG 567

QY 1679 AAGCATTTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721
DB 568 AAGCTTTTCTCGTGTATGAAAAGGTTTCACTCGTAG 610

Mon Apr 12 10:24:23 2004

us-09-508-377-10_copy_1058_3204.rmpb

Page 7

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Job time : 766.289 secs

Mon Apr 12 10:24:23 2004

us-09-508-377-10_copy_1058_3204.rst

Page 1

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 03:15:20 ; Search time 5665.27 Seconds
(without alignments)
11317.033 Million cell updates/sec

Title: US-09-508-377-10_COPY_1058_3204

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Scoring table: IDENTITY NUC
Gap 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
BST:*
1: em_estba:*
2: em_esthum:*
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6: em_estrpl:*
7: em_estro:*
8: em_hlc:*
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28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB	ID
1	238.2	11.1	623 14 CA726861
2	235	10.9	483 13 BQ239365
3	235	10.9	604 14 CD925132
4	223.8	10.4	577 13 CA025454

5	183.2	8.5	412	13	CA029212	CA029212 H264118F
6	150.2	7.0	297	14	CA500698	CA500698 WHE4022_D
7	136.6	6.4	219	12	BM441043	BM441043 EBEd02_SQ
8	135.8	6.3	831	14	CB629365	CB629365 OSIEB051
9	131.4	6.1	1006	29	CG421022	CG421022 ZMMBRC003
10	117.8	5.5	189	13	BQ754975	BQ754975 EBEd02_SQ
11	100.2	4.7	342	10	BE590829	BE590829 WHE085_F
12	98.6	4.6	517	13	BUE96927	BUE96927 H106F01F
13	98.6	4.6	556	9	AV913706	AV913706 AV913706
14	98.6	4.3	568	13	BQ240653	BQ240653 TAE05014F
15	92.6	4.3	139	12	BM368073	BM368073 EBEd01_SQ
16	90.8	4.2	2765	11	AY109521	AY109521 Zee MAY8
17	84.2	3.9	752	14	CD423046	CD423046 SAL_29_CO
18	81.2	3.8	830	28	CC421433	CC421433 PUFHML71TD
19	81.2	3.8	841	29	CC607582	CC607582 OG0BJ47TV
20	81.2	3.8	846	29	CC607572	CC607572 OG0BJ47TV
21	81.2	3.8	949	29	CG631299	CG631299 OG1CL07TV
22	81.2	3.8	949	29	CG340947	CG340947 OG3D139TV
23	80.8	3.8	806	28	AQ864199	AQ864199 nBE00022L
24	80.2	3.7	381	28	BZ407662	BZ407662 OGAAZ61TC
25	80.2	3.7	524	12	BG901327	BG901327 950003D05
26	80.2	3.7	561	13	BU099131	BU099131 3524_1_3
27	80.2	3.7	574	29	CG308966	CG308966 OGVC23TH
28	80.2	3.7	718	28	BZ538816	BZ538816 OGAEH26TC
29	80.2	3.7	720	28	BZ732892	BZ732892 OGEBD15TM
30	80.2	3.7	788	28	BZ644713	BZ644713 OGCA477TC
31	80.2	3.7	825	28	BZ732883	BZ732883 OGEBD15TC
32	80.2	3.7	844	29	CC730667	CC730667 OGFCX67TC
33	80.2	3.7	912	29	CG338761	CG338761 OGOC23TV
34	80.2	3.7	919	29	CG300534	CG300534 OGAAO47TV
35	80.2	3.7	928	29	CG199431	CG199431 PUFHML24TD
36	80.2	3.7	984	29	CG172191	CG172191 PUFHML11TB
37	77.6	3.6	410	29	CG732805	CG732805 119151CO
38	75.4	3.5	947	29	CG208838	CG208838 OG3B027TH
39	73.8	3.4	625	28	BZ775600	BZ775600 ih94d12_b
40	70.8	3.3	357	28	BZ644719	BZ644719 OGCA477TC
41	69	3.2	847	29	CG300518	CG300518 OGAAO47TH
42	67.6	3.1	480	9	AJ476662	AJ476662 AJ476662
43	67.6	3.1	480	9	AJ476662	AJ476662 AJ476662
44	67.4	3.1	693	28	BZ407668	BZ407668 OGAAZ61TM
45	64.8	3.0	388	12	BM443964	BM443964 EBEd09_SQ

ALIGNMENTS

RESULT 1
LOCUS CA726861 623 bp mRNA linear EST 26-NOV-2002
DEFINITION wdelF.pk002.g8 wdelF Triticum aestivum cDNA clone wdelF.pk002.g8 5'
end, mRNA sequence.
ACCESSION CA726861
VERSION CA726861.1 GI:25448761
KEYWORDS
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 623)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hairey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
Dumont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. Dupont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@usa.dupont.com
Seq primer: M13.
Location/Qualifiers

FEATURES

source
1. 623
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="wdef.pk002.g8"
/tissue_type="endosperm"
/lab_host="DH103"
/clone_lib="wdef"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: XhoI; Wheat (Triticum aestivum, Hi line) developing endosperm 2-7 DPA"

ORIGIN
Query Match 11.1%; Score 238.2; DB 14; Length 623;
Best Local Similarity 96.8%; Pred. No. 4e-40;
Matches 243; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 978 AGATACCTGAAGATATCGAGAGCAACCGCGGAAGTGAATGACAGAGGGGAGCTGCAG 1037
DB 283 AGATACCTGAAGATATCGAGAGCAACCGCGTGAATGACATGACAGGGGAGCCGACG 342
QY 1038 AGAACTTCAATCTTCAGAACCGACTCAGGCACTTGGAACAATCACTGATGTGTAA 1097
DB 343 AAAAACTTGAATCTTCAGAACCGACTCAGGCACTTGGAACAATCACTGATGTGTAA 402
QY 1098 CCAAGAGATTAAAGAACTAGTCTGTGGGAGAAACCGGAGTTTCCCAAAACCAAGAG 1157
DB 403 CCAAGAGATTAAAGAACTAGTCTGTGGGAGAAACCGGAGTTTCCCAAAACCAAGAG 462
QY 1158 ATGGGCGAATAATATACGAGATTGACCCCAACACATGAAAGATTTCCGAGGCACTTGACT 1217
DB 463 ATGGGCGAATAATATACGAGATTGACCCCAACACATGAAAGATTTCCGAGGCACTTGACT 522
QY 1218 ACCGTTAATGC 1228
DB 523 ACCGTTAATGC 533

RESULT 2
BQ239365 483 bp mRNA linear EST 03-MAY-2002
LOCUS TaE05031H05R TaE05 Triticum aestivum cDNA clone TaE05031H05R, mRNA
DEFINITION sequence.
ACCESSION BQ239365
VERSION BQ239365.1 GI:20435241
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triticaceae; Triticum.
1 (bases 1 to 483)
Cloutier, S.
Wheat functional genome - Glenlea developing seeds cDNA libraries unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-Food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@agr.gc.ca
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 031 row: H column: 05
Seq primer: M13 Reverse.
Location/Qualifiers
1. 483
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone="TaE05031H05R"

FEATURES
source

source
1. 604
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="rectal"
/db_xref="taxon:4565"
/clone="G75015P11"
/tissue_type="grain (750 degrees per day after pollination)"
/clone_lib="G750"

ORIGIN
Query Match 10.9%; Score 235; DB 14; Length 604;
Best Local Similarity 96.0%; Pred. No. 1.9e-39;

QY 978 AGATACCTGAAGATATCGAGAGCAACCGCGGAAGTGAATGACAGAGGGGAGCTGCAG 1037
DB 109 AGATACCTGAAGATATCGAGAGCAACCGCGTGAATGACATGACAGGGGAGCTGCAG 168
QY 1038 AGAACTTCAATCTTCAGAACCGACTCAGGCACTTGGAACAATCACTGATGTGTAA 1097
DB 169 AAAAACTTGAATCTTCAGAACCGACTCAGGCACTTGGAACAATCACTGATGTGTAA 228
QY 1098 CCAAGAGATTAAAGAACTAGTCTGTGGGAGAAACCGGAGTTTCCCAAAACCAAGAG 1157
DB 229 CCAAGAGATTAAAGAACTAGTCTGTGGGAGAAACCGGAGTTTCCCAAAACCAAGAG 288
QY 1158 ATGGGCGAATAATATACGAGATTGACCCCAACATGAAAGATTTCCGAGGCACTTGACT 1217
DB 289 ATGGGCGAATAATATACGAGATTGACCCCAACATGAAAGATTTCCGAGGCACTTGACT 348
QY 1218 ACCGTTAATGC 1228
DB 349 ACCGTTAATGC 359

RESULT 3
CD925132 604 bp mRNA linear EST 15-JUL-2003
LOCUS G750.115P11F010709 G750 Triticum aestivum cDNA clone G750115P11,
DEFINITION mRNA sequence.
ACCESSION CD925132
VERSION CD925132.1 GI:36772896
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triticaceae; Triticum.
1 (bases 1 to 604)
Genoplante, a major partnership french program in plant genomics
Unpublished (2002)
Contact: Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genome programme 'genoplante' (<http://www.genoplante.com> and <http://genoplante-info.info.genogen.fr>).
Location/Qualifiers
1. 604
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="rectal"
/db_xref="taxon:4565"
/clone="G75015P11"
/tissue_type="grain (750 degrees per day after pollination)"
/clone_lib="G750"

ORIGIN
Query Match 10.9%; Score 235; DB 14; Length 604;
Best Local Similarity 96.0%; Pred. No. 1.9e-39;

cloning system used Blue/white selection for recombinants
is not 100% reliable. Average insert size is 900 bp

ORIGIN

Query Match 8.5%; Score 183.2; DB 13; Length 412;
Best Local Similarity 93.6%; Pred. No. 2e-28; Indels 0; Gaps 0;
Matches 191; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1025 GGGGGAGCTGCAGAGAACTTCATCTTCAGAACCGACTGAGGGCTTTGGAAACATC 1084
Db 1 GGGGGGCTGCAGAGAACTTCATCTTCAGAACCGACTGAGGGCTTTGGAAACATC 60
QY 1085 ACTGATGTGTAACTCAAGAGATTAGGAACTAGTGTGGGGGAGAAACCGGAGTTGTC 1144
Db 61 ACTGATGTGTAACTCAAGAGATTAGGAACTAGTGTGGGGGAGAAACCGGAGTTGTC 120
QY 1145 CCAAAACAGAGATGGGCGAGAAATATAGAGATTGACCCACACAGAAAGATTTCGG 1204
Db 121 CCAAAACAGAGATGGGCGAGAAATATAGAGATTGACCCACAGCTGAAAGATTTCGG 180
QY 1205 AGCCATCTTACTACCGGTAATGC 1228
Db 181 AGCCATCTTACTACCGTAATGC 204

RESULT 6 297 bp mRNA linear EST 14-NOV-2002
CA500698
LOCUS WHE4023_D10.H19PT wheat meiotic anther cDNA library Triticum
DEFINITION WHE4023_D10.H19PT wheat meiotic anther cDNA library Triticum
ACCESSION CA500698
VERSION CA500698.1 GI:24991658
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 297)
Anderson, O.D., Chao, S., Crossman, C., Langridge, P., Lazo, G.R.,
Pham, J., Rausch, C.J., Sutton, T., Woo, J. and Wilson, C.
The structure and function of the expressed portion of the wheat
genomes - Meiotic anther cDNA library
Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105959773
Fax: 5105959818
Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: 17 primer.
Location/Qualifiers

FEATURES
source 1..297
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE4023_D10.H19"
/tissue_type="Anther"
/dev_stage="Meiotic stages pre-meiosis-metaphase I"
/lab_host="E. coli DH10B"
/clone_lib="Wheat meiotic anther cDNA library"
/note="Vector: pSPORT1, Site 1: SalI; Site 2: NotI; Plants
were grown in a glasshouse. Anther meiotic stage was
determined by removing anthers from individual primary
florets. One anther was sacrificed for microscopic
staging, and if determined to be between (and including)
meiotic stages pre-meiosis and metaphase I, the remaining
two anthers were collected and pooled for library
construction. The tissue, total RNA, and poly(A) RNA were

ORIGIN

Query Match 7.0%; Score 150.2; DB 14; Length 297;
Best Local Similarity 85.6%; Pred. No. 2.1e-21; Indels 0; Gaps 0;
Matches 167; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CGCCAGCTTCCACCCCGCGACACGTTGCTCCCTTCATCGCTTCTCAATTATA 60
Db 3 CGCCAGCTTCCACCCCGCGACACGTTGCTCCCTTCATCGCTTCTCAATTATA 62
QY 61 TCTCCATCACTGGGTTCCGCGCTGCATTTCGCGCGCGGTTGAGTGAATCTGGCGCA 120
Db 63 TCTCCATCACTGGGTTCCGCGCTGCATTTCGCGCGCGGTTGAGTGAATCTGGCGCA 122
QY 121 CTGCTGACTCATATCACTACGCGGGGATGCGGACGTTCCGCGCGGACCTTCG 180
Db 123 CTGACCGACTCACTCGCTGCGCGGGGATGCGCGCGGTTGAGTGAATCTGGCGCG 182
QY 181 GTGTGGCGCGGCGCG 195
Db 183 GTGTGGCGCGGCGCG 197

RESULT 7 219 bp mRNA linear EST 23-JUL-2002
BM441043
LOCUS EBed02_SQ002_E01.R endosperm, 8 DPA, no treatment, cv Optic, Ebed02
DEFINITION EBed02_SQ002_E01.R endosperm cDNA clone EBed02_SQ002_E01.5', mRNA
ACCESSION BM441043
VERSION BM441043.2 GI:21932253
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 219)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudge, S., Cardie, L.,
Ramsey, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
On Feb 1, 2002 this sequence version replaced gi:18471818.
Contact: Waugh, R., Marshall, D.F.
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
All sequence has a phred quality score of 20 or over
Seq primer: M13 reverse.
Location/Qualifiers

FEATURES
source 1..219
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Optic"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBed02_SQ002_E01"
/tissue_type="endosperm"
/dev_stage="8 DPA"
/lab_host="DH10B"
/clone_lib="endosperm, 8 DPA, no treatment, cv Optic,
EBed02"
/note="Vector: pSPORT1, Site 1: Sal I, Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.

prepared, cDNA synthesised, and directionally ligated into
pSPORT1 by Tim Sutton in the P Langridge Lab at the
Department of Plant Science, University of Adelaide, Waite
Campus, Australia. Average insert size 1.5Kb. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

Derived from endosperm tissue dissected from developing grains (8 days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BSRG/SEBRAD funded cereal IGP (Investigating Gene Function) project."

ORIGIN

Query Match 6.4%; Score 136.6; DB 12; Length 219;
Best Local Similarity 88.2%; Pred. No. 1.6e-18;
Matches 172; Conservative 0; Mismatches 19; Indels 4; Gaps 2;

QY 90 TCGCCGGCGGGTTGATGAGATCTGGGCGACTGCTGACTCAATCAACGCGG-GAT 148
DB 9 TGGGCGGGGTTGATGAGATCTGGGCGACCGACCTGCTGCTGCTGCGGGAGAT 68
QY 149 GCGGACGTTCCGGGTCTCCGGCGGCACTCTCGGTGGGGCGGGCGGCGGAG---T 205
DB 69 GCGGACGTTCCGGGTCTCCGGCGGCACTCTGTTGGGGCGGGCGGCGGAGGCGCT 128
QY 206 GCGCGGGCGGCTCGAGCGAGCGGGCGGCGGCGGCTGCTGCTGCTGCTGAGAA 265
DB 129 GCGGCGATCCGGCTCGAGCGAGGCGGGCGGCTGCTGCTGCTGCTGCTGAGAA 188
QY 266 GAAGGACTCTCTCG 280
DB 189 GAAGGACTCTCTCG 203

RESULT 8
LOCUS CB629365 831 bp mRNA linear EST 08-APR-2003
DEFINITION OS11B05120.f OS11B Oryza sativa (indica cultivar-group) cDNA
ACCESSION CB629365
VERSION CB629365.1 GI:29624354
SOURCE EST.
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 831)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wang,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)

JOURNAL COMMENT
TITLE
AUTHORS
CONTACT: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

PCR PRIMERS
FORWARD: gta aac cga cgg cca cta g
BACKWARD: gga aac agc tat gac cat g
Plate: 05 Row: 1 Column: 20
Seq primer: gta aac cga cgg cca cta g
Location/Qualifiers
1. .831
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39946"
/clone="OS11B05120"
/tissue_type="leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_id="OS11B"
/note="Vector: pBlueScript II KS+; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (P06-6-3)"

ORIGIN

Query Match 6.3%; Score 135.8; DB 14; Length 831;
Best Local Similarity 76.3%; Pred. No. 2.9e-18;
Matches 167; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1006 GGGGGAATGTAACATGACAGGGGGAGTGGCGAGAACTTCATCTTCAGAACCACTCA 1065
DB 90 GCGAAGAGCAAGCAATTAAGTTGTTGGCTGAGAGCAAACTTGAATCTTCAGAACTTCA 149
QY 1066 GGGCATTTGGAAACAATCACTGATGTGTATCCAAAGAGTTAAGAACTAGTGTGG 1125
DB 150 AGACATTGAGAAATATGATGATGAGGGGTGATCAAAATGCTGATGAACCAACTGTGA 209
QY 1126 GAGAAACCGGAGTTGTCCCAAAACCGAGATGGCGAATAATATACGAATTGACCC 1185
DB 210 GGATTAACCAAGATTATCCCAACCAAGAGATGGCGAAGATATACCAATATGACCC 269
QY 1186 AACCTGAATTTTGGAGCCATCTTGAATCCGTA 1224
DB 270 AATCTGAAGAGATTGGAACCAATCTTGAATCCGTA 308

RESULT 9
CG421022/c 1006 bp DNA linear GSS 22-SEP-2003
LOCUS ZMMBBC0034G11f ZMMBBC (EcoRI) Zea mays subsp. mays genomic clone
DEFINITION ZMMBBC0034G11 5', genomic survey sequence.
ACCESSION CG421022
VERSION CG421022.1 GI:34565867
SOURCE GSS.
ORGANISM Zea mays subsp. mays (maize)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 1006)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wang,R. and Messing,J.
Sequencing of the maize genome at PGR (2003c)
Unpublished (2003)
CONTACT: Bharti,A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: 17
Class: BAC ends
High quality sequence start: 106.
Location/Qualifiers
1. 1006
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="B73"
/sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMMBBC0034G11"
/lab_host="E. coli DH10B"
/clone_id="ZMMBBC (EcoRI)"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI"

REFERENCE
AUTHORS
TITLE
JOURNAL COMMENT
CONTACT: Bharti,A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: 17
Class: BAC ends
High quality sequence start: 106.
Location/Qualifiers
1. 1006
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="B73"
/sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMMBBC0034G11"
/lab_host="E. coli DH10B"
/clone_id="ZMMBBC (EcoRI)"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI"

FEATURES
source
1. 1006
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="B73"
/sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMMBBC0034G11"
/lab_host="E. coli DH10B"
/clone_id="ZMMBBC (EcoRI)"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI"

ORIGIN

Query Match 6.1%; Score 131.4; DB 29; Length 1006;
Best Local Similarity 60.1%; Pred. No. 2.6e-17;
Matches 331; Conservative 0; Mismatches 176; Indels 44; Gaps 5;

QY 1597 TGGGTATACCTCGGTGATTCACAGATACAGGAATACAGGAATTCGTCGCTATT 1656
DB 782 TTGGTTGCTTTTGTGATTCACAGATACAGGAATACAGGAATTCGTCGCTATT 723

QY 1657 GACCAATGAAAGTGATGGAAGCATTTTCTGCTGATATGAAAGCTTGATTTAC 1716
 DB 722 GATCAACATGAAGTGCTGTTGGATGATTTTCAAGCGGTACGAAAGCTTGATTTACT 663
 QY 1717 CGCAGGTAATTTAAAGCTTTATTTATGAAAGCGCTCCAGCTAGTCTAATGCAATCT 1776
 DB 662 CGCAGGTAATTTAAAGCTTTATTTATGAAAGCGCTCCAGCTAGTCTAATGCAATCT 609
 QY 1777 TATAGAAATTTATATTCCTGTTTCCCTCTCTTTTCCAGTGTGAGGATAGT 1836
 DB 608 TATAGCAAAATGATGATTAAC---TGTTTCCCTCTCTTTTCCAGCGGTAGAGATTC-- 554
 QY 1837 CTAAATGCAATCTTATAGAAATTTATATTCCTGTTTCCCTAATTTCCAGTGTGA 1896
 DB 553 -----ACTTACAGAGATGGGCTCTGAGCATGATGATGTTCTCACAGATTT 505
 QY 1897 AGGTATCATTTACCGAATGGGCTCCCTGAGCGCATGATGTTCTTTTAAAGTTCTT 1956
 DB 504 GGCAGTCACCTTTTAAACACATGAT-----AGTTTCATATTCATCTGTTTACCTTGTG 451
 QY 1957 AAGAGACACCTTCCAAATTTATTTGTTATGCTACTATTCACCAACTAGTACTGACT 2016
 DB 450 CGCAATACAGACAGATGATTTACACGATATTCAGATTTCTTCAAAAGATATGTTTA 391
 QY 2017 TACAATTAAGTCTACTGAAATGACGACGATTAATAATTATGATCTGCTTTTGAC 2076
 DB 390 T-----CTTCTGATCAACTCATTTAAGATTTAAGAACGGGTTCTTACAT 347
 QY 2077 CTTGTTACGTTCTGACGATTAAGTACTGATTTCAACAATTTGAAATCCAAATGCGATAC 2136
 DB 346 CTTACTCAGCTCTCAGCAGATAGAAAGTACTTCAACAATGGAACCCAAATGCTGATGC 287
 QY 2137 TATGACCAAG 2147
 DB 286 TATGCCAGAG 276

RESULT 10
 BO754975 189 bp mRNA linear EST 26-JUL-2002
 LOCUS Ebed02_S0003_F18_R endospem, 8 DPA, no treatment, cv Optic, Ebed02
 DEFINITION Hordeum vulgare subsp. vulgare cDNA clone Ebed02_S0003_F18 5', mRNA
 sequence.
 ACCESSION BO754975
 VERSION BO754975.1 GI:21963447
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 1 (bases 1 to 189)
 Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,
 Ramsay, L., Machray, G., Marshall, D.F.M., and Waugh, R.
 TITLE Development of Barley Transcriptome Resources
 JOURNAL Unpublished (2001)
 COMMENT Contact: Maugh R. Marshall, DF
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: est@scri.sari.ac.uk.
 FEATURES
 source location/Qualifiers
 1..189
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Optic"
 /sub_species="vulgare"
 /db_xref="taxon:11509"
 /clone="Ebed02_S0003_F18"
 /issue_type="endospem"
 /dev_stage="8 DPA"

ORIGIN
 Query Match 5.5%; Score 117.8; DB 13; Length 189;
 Best Local Similarity 87.9%; Pred. No. 1.6e-14;
 Matches 152; Conservative 0; Mismatches 17; Indels 4; Gaps 2;
 /lab_host="DH10B"
 /clone_lib="endospem, 8 DPA, no treatment, cv Optic,
 Ebed02"
 /note="vector: pSPOR1; Site 1: Sal I; Site 2: Not I;
 Non-normalised library, directionally cloned into pSPOR1.
 Derived from endospem tissue dissected from developing
 grains (8 days post anthesis) in glasshouse grown barley
 plants. Developed as part of the barley transcriptome
 resources of BSRC/SERAD funded cereal IGF (Investigating
 Gene Function) project."

QY 112 TCTGGCGCACTGCTGACTCAATCACTACGCGGG-GATGGCAAGTTCCGGGTCCGGC 170
 DB 1 TCTGGCGCAAGCACTGCTGCTGCTGCGCGGAGATGGCAGTTCGGGTCTCCGGC 60
 QY 171 GCGACTCTGCTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 227
 DB 61 GCGACCTTGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 QY 228 AAGGGGCGGGCGGACTTGGCGGCTGCTCTCTCAGAGAGAGAGACTCTCTCG 280
 DB 121 AAGGGGCGGGCGGACTTGGCGGCTGCTCTCTCAGAGAGAGAGACTCTCTCG 173

RESULT 11
 BE590829 342 bp mRNA linear EST 18-AUG-2000
 LOCUS WHE0855_F05_K09ZS wheat 20-45 DAP spike cDNA library Triticum
 DEFINITION aestivum cDNA clone WHE0855_F05_K09, mRNA sequence.
 ACCESSION BE590829
 VERSION BE590829.1 GI:9845902
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 342)
 Anderson, O.D., Cho, S., Choi, D.W., Close, T.J., Fenton, R.D.,
 Han, P.S., Heia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rauech, C.J.,
 Seaton, C.L. and Tong, J.C.
 TITLE The structure and function of the expressed portion of the wheat
 JOURNAL Genomes - 20-45 DAP spike cDNA library
 COMMENT Unpublished (2000)
 CONTACT: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 510595773
 Fax: 510595818
 Email: oanderson@wars.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seg primer: Strategene SK primer.
 FEATURES
 source location/Qualifiers
 1..342
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE0855_F05_K09"
 /issue_type="Spike and seed"
 /dev_stage="Adult plant"
 /lab_host="E. coli SOLR"
 /clone_lib="Wheat 20-45 DAP spike cDNA library"
 /note="vector: Lambda Uni-ZAP XR, excised phageid;
 Site 1: EcoRI; Site 2: XhoI; PRs were grown in the
 greenhouse. Spikes at 20 DAP and seeds at 30

we harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give Bluescript phagemids in the Tj Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

ORIGIN

Query Match 4.7%; Score 100.2; DB 10; Length 342;
Best Local Similarity 97.1%; Pred. No. 1e-10; 3; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 3;

1617 CACAGATACAGCGAATACAGAGAAATTCGTCTGCTATTGACCAACATGAAGGTGATT 1676
17 CTACCGATACAGGAATACAGAGAAATTCGTCTGCTATTGACCAACATGAAGGTGATT 76

QY 1677 GGAAGCATTTTCTCGTGTATTGAAAAGCTTGATTTACCCGCAG 1721

DB 77 GGAAGCATTTTCTCGTGTATTGAAAAGCTTGATTTACCCGCAG 121

RESULT 12 517 bp mRNA linear EST 23-OCT-2002
BU996927 H106F01r HI Hordeum vulgare subsp. vulgare cDNA clone H106F01
LOCUS 5-PRIME, mRNA sequence.
DEFINITION BU996927.1 GI:24273910

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 517)
Zhang, H., Meschke, W., Michalek, W., Stein, N. and Gruner, A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils

Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595

Email: stein@ipk-gatersleben.de
Insert Length: 517 Std Error: 0.00
Plate: 6 Row: F Column: 1
Seq primer: M13rev.

FEATURES

source

1..517
Location/Qualifiers
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/cuiivar="barke"
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/db_xref="GABI:250791"
/db_xref="taxon:112509"
/clone="H106F01"
/tissue_type="female inflorescences"
/dev_stage="female inflorescences (approx. 3 mm in size)"
/lab_host="Xl10-Gold"
/clone_lib="HI"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN

Query Match

4.6%; Score 98.6; DB 13; Length 517;

Best Local Similarity 96.2%; Pred. No. 2.3e-10;
Matches 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1617 CACAGATACAGCGAATACAGAGAAATTCGTCTGCTATTGACCAACATGAAGGTGATT 1676
DB 29 CTACCGATACAGGAATACAGAGAAATTCGTCTGCTATTGACCAACATGAAGGTGATT 88

QY 1677 GGAAGCATTTTCTCGTGTATTGAAAAGCTTGATTTACCCGCAG 1721

DB 89 GGAAGCATTTTCTCGTGTATTGAAAAGCTTGATTTACCCGCAG 133

RESULT 13 556 bp mRNA linear EST 18-JAN-2002
AV913706
LOCUS AV913706 K. Sato unpublished cDNA library, cv. Haruna Nijo
DEFINITION germination shoots Hordeum vulgare subsp. vulgare cDNA clone
bag823a09 5', mRNA sequence.
AV913706

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 556)
Sato, K., Saito, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadao Shin-i

Center for Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

Location/Qualifiers
1..556
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/clone_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo germination shoots"

FEATURES

source

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/dev_stage="germination"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo germination shoots"

ORIGIN

Query Match 4.6%; Score 98.6; DB 9; Length 556;
Best Local Similarity 96.2%; Pred. No. 2.4e-10;
Matches 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1617 CACAGATACAGCGAATACAGAGAAATTCGTCTGCTATTGACCAACATGAAGGTGATT 1676
DB 21 CTACCGATACAGGAATACAGAGAAATTCGTCTGCTATTGACCAACATGAAGGTGATT 80

QY 1677 GGAAGCATTTTCTCGTGTATTGAAAAGCTTGATTTACCCGCAG 1721

DB 81 GGAAGCATTTTCTCGTGTATTGAAAAGCTTGATTTACCCGCAG 125

RESULT 14 568 bp mRNA linear EST 03-MAY-2002
BQ240653
LOCUS BQ240653
DEFINITION Tab05014F06R Tab05 Triticum aestivum cDNA clone Tab05014F06R, mRNA
sequence.
BQ240653

ACCESSION
VERSION
KEYWORDS
SOURCE
BQ240653.1 GI:20436529
Triticum aestivum (bread wheat)

ORGANISM

REFERENCE

COMMENT

inos

0000

Matches

Dib

Db

BM368073

•

SOURCE

1

TITLE

Triticum aestivum
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poidea; Triticeae; Triticum.
 1 (bases 1 to 568)
 Cloutier,S.
 Wheat functional genomics - Glenlea developing seeds cDNA libraries
 unpublished (2002)
 Contact: Dr. Sylvie Cloutier
 Central Research Centre, Agriculture and Agri-food Canada
 195 Dufour Rd. Winnipeg, MB, Canada R3T 2M5
 Tel: (204) 983-2340
 Fax: (204) 983-4604
 Email: scloutier@agr.gc.ca
 was cloned directionally, not all sequences generated with reverse
 primer were from the 5' end (same with forward primer and 3' end).
 Average insert size is >2.0 kb
 plate: 014 row: F column: 06
 Seq primer: M13 Reverse.
 Location/Qualifiers
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 /tissue_type="developing seeds"
 /dev_stage="5 days after anthesis"
 /lab_host="E. coli DH10B"
 /clone_lib="TA0505"
 /note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
 NotI; Site_2: MluI; mRNA obtained from wheat seeds of
 cultivar Glenlea 5 days post-anthesis"
 4.6%; Score 98.6; DB 13; Length 568;
 1 Similarity 96.2%; Pred. No. 2.4e-10;
 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 17 CAACAGATACGCGAATACAGAGATTGCTGCTATTGACCAACATGAAGTGATT 16766
 38 CTACCGATACAGGAAATCAAGAGATTCGTCGCTATTGACCAACTGAAGCGATT 97
 577 GGAAGCATTTCTGCTGTTATGAAGAAGCTGATTAACCGCAG 1721
 98 GGAAGCATTTCTGCTGTTATGAAGAAGCTGATTAACCGCAG 142
 BM368073 139 bp mRNA linear EST 23-JUL-2002
 Ebedot1_S0002_B11_R endsepem, 6 DPA, no treatment, cv Optic, Ebedot1
 Hordeum vulgare subsp. vulgare cDNA clone Ebedot1_S0002_B11 5', mRNA
 sequence.
 BM368073
 BM368073.1 GI:1811463
 EST.
 Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Poidea; Triticeae; Hordeum.
 1 (bases 1 to 139)
 Helley,P., Izu,H., Caldwell,D., McCallum,N., Mudie,S., Cardie,L.,
 Ramey,L., Machray,G., Marshall,D.F.M. and Maugh,R.
 Development of barley transcriptome Resources
 Unpublished (2001)
 Contact: Waugh R, Marshall DF
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731

nos

○

●

►

1

```

Email: est@scri.sari.ac.uk
All sequence has a phred quality score of 20 or over
Seq primer: M13 reverse.
Location/Qualifiers
1..139
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/mol_type="mRNA"
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/tissue_type="endosperm"
/dev_stage="6 DPA"
/lab_host="DH10B"
/clone_lib="endosperm, 6 DPA, no treatment, cv Optic,
EBead01"
/note="Vector: pSPORT1; Site1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1
Derived from endosperm tissue dissected from developing
grains (6 days post anthesis) in glasshouse grown barley
plants. Developed as part of the barley transcriptome
resources of BBSRC/SERAD funded cereal IGF (Investigating
Gene Function) project."
ch 4.3%; Score 92.6; DB 12; Length 139;
111 Similarity 90.2%; Pred. No. 3.7e-09;
111, Conservative 0; Mismatches 9; Indels 3; Gaps 1;
61 GGTGTCGGGCGCGCACTCTCGGTGTGAGCGCGGCGCGCGAG--TGCGCGGCGCGG 217
1 GGTGTCGGGCGCGCACTCTGTGTGTGAGCGCGGCGCGCGAGCGCTGCCGCATCCGG 60
118 CTCGAGCGGAGGGGCGCGGCGGCACTTGCCGTGCTGCTCTCTCAGAAAGAACTCTCT 277
61 CTCGAGCGGAGGGGCGCGGCGGCACTTGCCGTGCTCTCTCTCAGAAAGAACTCTCTC 120
278 TCG 280
121 TCG 123

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Search completed: April 10, 2004, 14:06:19
Job time : 5678.27 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 01:54:35 ; Search time 8035.73 Seconds

(without alignments)
11057.263 Million cell updates/sec

Title: US-09-508-377-10_COPY_4818_6867

Sequence: 1 ccgaagaataatcatatgc.....catgtgcgaagatgaagtg 2050

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_or:*
21: em_ox:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_scs:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_in:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_red:*
36: em_hcg_man:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_higo_hum:*
40: em_higo_mus:*
41: em_higo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2050	100.0	11463	6	AX031271	AX031271 Sequence
2	2025	98.8	11475	8	AF338431	AF338431 Aegilops
3	250.8	12.2	691	8	AY235709	AY235709 Zea mays
4	250.8	12.2	693	8	AY235691	AY235691 Zea mays
5	250.8	12.2	693	8	AY235701	AY235701 Zea mays
6	250.8	12.2	712	8	AY235702	AY235702 Zea mays
7	250.8	12.2	713	8	AY235690	AY235690 Zea mays
8	250.8	12.2	713	8	AY235692	AY235692 Zea mays
9	250.8	12.2	713	8	AY235693	AY235693 Zea mays
10	250.8	12.2	713	8	AY235694	AY235694 Zea mays
11	250.8	12.2	713	8	AY235695	AY235695 Zea mays
12	250.8	12.2	713	8	AY235696	AY235696 Zea mays
13	250.8	12.2	713	8	AY235697	AY235697 Zea mays
14	250.8	12.2	713	8	AY235698	AY235698 Zea mays
15	250.8	12.2	713	8	AY235703	AY235703 Zea mays
16	250.8	12.2	713	8	AY235704	AY235704 Zea mays
17	250.8	12.2	713	8	AY235705	AY235705 Zea mays
18	250.8	12.2	713	8	AY235706	AY235706 Zea mays
19	250.8	12.2	713	8	AY235707	AY235707 Zea mays
20	250.8	12.2	713	8	AY235708	AY235708 Zea mays
21	250.8	12.2	713	8	AY235710	AY235710 Zea mays
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23	250.8	12.2	713	8	AY235713	AY235713 Zea mays
24	250.8	12.2	713	8	AY235714	AY235714 Zea mays
25	250.8	12.2	713	8	AY235715	AY235715 Zea mays
26	250.8	12.2	23449	8	AF072725	AF072725 Zea mays
27	248.8	12.1	713	8	AY235711	AY235711 Zea mays
28	244	11.9	639	8	AY235700	AY235700 Zea mays
29	240.4	11.7	621	8	AY235699	AY235699 Zea mays
30	226.6	11.1	624	8	AY290243	AY290243 Zea mays
31	226.2	11.0	626	8	AY290221	AY290221 Zea mays
32	226.2	11.0	627	8	AY290293	AY290293 Zea mays
33	225.6	11.0	627	8	AY290222	AY290222 Zea mays
34	225.6	11.0	626	8	AY290268	AY290268 Zea mays
35	225.6	11.0	627	8	AY290242	AY290242 Zea mays
36	225.6	11.0	627	8	AY290244	AY290244 Zea mays
37	225.6	11.0	627	8	AY290300	AY290300 Zea mays
38	225	11.0	626	8	AY290215	AY290215 Zea mays
39	225	11.0	626	8	AY290217	AY290217 Zea mays
40	225	11.0	626	8	AY290227	AY290227 Zea mays
41	225	11.0	626	8	AY290256	AY290256 Zea mays
42	225	11.0	626	8	AY290259	AY290259 Zea mays
43	225	11.0	626	8	AY290260	AY290260 Zea mays
44	225	11.0	626	8	AY290261	AY290261 Zea mays
45	225	11.0	626	8	AY290265	AY290265 Zea mays

ALIGNMENTS

RESULT 1
AX031271 11463 bp DNA linear PAT 20-SEP-2000
LOCUS AX031271
DEFINITION Sequence 10 from Parent W09914314.
ACCESSION AX031271
VERSION AX031271.1 GI:10278603
KEYWORDS
SOURCE
ORGANISM
Aegilops tauschii
Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Aegilops.
REFERENCE
Li Z., Morell M. and Rahman S.
1
Regulation of gene expression in plants

JOURNAL Patent: WO 9914314-A 10 25-MAR-1999;
GOODMAN FIELDER LTD (AU) ; LI ZHONGYI (AU) ;
RAHMAN SAEDEUR (AU) ; UNIT AUSTRALIAN (AU) ; COMM SCIENT IND RES
ORG (AU) ; GROUPE L'IMAGRAIN PACIFIC PTE L (AU)

FEATURES
source
1..11463
Location/Qualifiers

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II GENE"

ORIGIN

Query Match 100.0%; Score 2050; DB 6; Length 11463;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2050; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGAGATTAATTGATGCTAATTTTGGGATGAGGTGTCACAGAAATTAAGGCTT 60
DB 4818 CCGAGATTAATTGATGCTAATTTTGGGATGAGGTGTCACAGAAATTAAGGCTT 4877
QY 61 GGATACATGCAATGAGATGATGCAATCCAGAGCAATTCATATGCAAGCTTTGGG 120
DB 4878 GGATACATGCAATGAGATGATGCAATCCAGAGCAATTCATATGCAAGCTTTGGG 4937
QY 121 TATTCACAAATCCATTTTCTGTATACACTTACCCATTTGGAGCTTAAATACC 180
DB 4938 TATTCACAAATCCATTTTCTGTATACACTTACCCATTTGGAGCTTAAATACC 4997
QY 181 TATGCTCATGCAATTAATAATTTGGATATATCTTATTAGATATAGTACAAT 240
DB 4998 TATGCTCATGCAATTAATAATTTGGATATATCTTATTAGATATAGTACAAT 5057
QY 241 ACACTTAGATTTGCAAAAAGATCATTTTATGTGTGGCTTTCCAGGTACATGTT 300
DB 5058 ACACTTAGATTTGCAAAAAGATCATTTTATGTGTGGCTTTCCAGGTACATGTT 5117
QY 301 ACTAATTTTTTGCACCAAGTAGCCGCTTTGGAACTCCAGAGCACTTAAATCCTTATC 360
DB 5118 ACTAATTTTTTGCACCAAGTAGCCGCTTTGGAACTCCAGAGCACTTAAATCCTTATC 5177
QY 361 GATAGACACATGAGCTGTGGTTGCTGTCTTATGATATTTGTCATAGGTAATTAATC 420
DB 5178 GATAGACACATGAGCTGTGGTTGCTGTCTTATGATATTTGTCATAGGTAATTAATC 5237
QY 421 CAATTTAATTTAGCTGTTTAACTGTTTATCTGTTATCTTAAAGGAAATTCAGGCAAT 480
DB 5238 CAATTTAATTTAGCTGTTTAACTGTTTATCTGTTATCTTAAAGGAAATTCAGGCAAT 5297
QY 481 ATATATACATTTGCAAAAGCTAAGGTGGCCAAAGTGAATTCGAAAATCTGAGAGGAT 540
DB 5298 ATATATACATTTGCAAAAGCTAAGGTGGCCAAAGTGAATTCGAAAATCTGAGAGGAT 5357
QY 541 AAGGAAATTTGGCAAAACTAGAGTGGCAAAAATTAATTTTCCATCTTAATGGCAGG 600
DB 5358 AAGGAAATTTGGCAAAACTAGAGTGGCAAAAATTAATTTTCCATCTTAATGGCAGG 5417
QY 601 GCCCTATGCGCAATATTTTTCATTTCTATATTAATTTGTCAGTGTGCTTTTTCCTC 660
DB 5418 GCCCTATGCGCAATATTTTTCATTTCTATATTAATTTGTCAGTGTGCTTTTTCCTC 5477
QY 661 AGATGTTTAAACCAAGTTGCAATGAATATGATTTGGTACATGTAATCAACAGAGTTC 720
DB 5478 AGATGTTTAAACCAAGTTGCAATGAATATGATTTGGTACATGTAATCAACAGAGTTC 5537
QY 721 CATAGAAATATGTTTGTATGGAACAATTTGATCCATAGATGAGTGGATTGGAAGT 780
DB 5538 CATAGAAATATGTTTGTATGGAACAATTTGATCCATAGATGAGTGGATTGGAAGT 5597
QY 781 TCAAGTGTCTATCAATAGATTAATCACTGGCCATGATCTGTGGCACTACATATATGTT 840

DB 5598 TCAAGTGTCTATCAATAGATTAATCACTGGCCATGATCTGTGGCACTACATATATGTT 5657
QY 841 GCAAGTTGAAAACCTGACAGCAATACCTCACTGATTAAGTGGCCAGGCCCACTTGGCAGC 900
DB 5658 GCAAGTTGAAAACCTGACAGCAATACCTCACTGATTAAGTGGCCAGGCCCACTTGGCAGC 5717
QY 901 TTGATCTAGATGTTACTTCCCTGTTGTAATTCATTTGAACATATTTACTTAAGTTCTTCA 960
DB 5718 TTGATCTAGATGTTACTTCCCTGTTGTAATTCATTTGAACATATTTACTTAAGTTCTTCA 5777
QY 961 TTTTGTCCCAATGCAAACTCTTTAAGTTTGAACCAAGTCTATGGAATATATCAATC 1020
DB 5778 TTTGTCTTCAATGCAAACTCTTTAAGTTTGAACCAAGTCTATGGAATATATCAATC 5837
QY 1021 TACAACAACAATTAATCTTGAATGCAATTAACAATTTTATTTATATATAGACATCT 1080
DB 5838 TACAACAACAATTAATCTTGAATGCAATTAACAATTTTATTTATATATAGACATCT 5897
QY 1081 TTGATGTTGATGATGCAACATTTTCTATAGCTTGTCAAAATATAGAGATTGGA 1140
DB 5898 TTGATGTTGATGATGCAACATTTTCTATAGCTTGTCAAAATATAGAGATTGGA 5957
QY 1141 CTTGAGCAAAATCTAGAACTTCAATCAATTTGGATCAGAGGGAACATCAATATATAGA 1200
DB 5958 CTTGAGCAAAATCTAGAACTTCAATCAATTTGGATCAGAGGGAACATCAATATATAGA 6017
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DB 6018 TAGATGTCAACACTTCAACAAAAAATGAGACCTTGTCCACATATATGATCAGACATC 6077
QY 1261 TGTGTTGCTTTAGCCACTTGTTCATATTTATGTGTGTTGTACTATCTACTTTCTTC 1320
DB 6078 TGTGTTGCTTTAGCCACTTGTTCATATTTATGTGTGTTGTACTATCTACTTTCTTC 6137
QY 1321 TACTTGGTTGGTATATCTATTTCACTGCAATGCTGATCAATGATTTGTGACCT 1380
DB 6138 TACTTGGTTGGTATATCTATTTCACTGCAATGCTGATCAATGATTTGTGACCT 6197
QY 1381 GCAGTCATCTGCTCAATAATAATACCTTGAAGCTTTGATGATGTTGATGCACTGATAC 1440
DB 6198 GCAGTCATCTGCTCAATAATAATACCTTGAAGCTTTGATGATGTTGATGCACTGATAC 6257
QY 1441 ATTACTTCCAGGTGCTCCAGCGGCACTGATGATGATGATGATGATGATGATGATGAT 1500
DB 6258 ATTACTTCCAGGTGCTCCAGCGGCACTGATGATGATGATGATGATGATGATGATGAT 6317
QY 1501 ATGGAGTTGGGAAGTATGATCTGACTTCTGTGACCAATTTTGGCTAAGCTTCTCTG 1560
DB 6318 ATGGAGTTGGGAAGTATGATCTGACTTCTGTGACCAATTTTGGCTAAGCTTCTCTG 6377
QY 1561 TTAATCTGTTCTTACACATGTTGATATTTCTATTTTATGAGATTTTGAATTTCTA 1620
DB 6378 TTAATCTGTTCTTACACATGTTGATATTTCTATTTTATGAGATTTTGAATTTCTA 6437
QY 1621 TCAAAACGAGATGCTGCTTGAAGATATTAAGTTTGAATGATTTTGAATTTGATGAGG 1680
DB 6438 TCAAAACGAGATGCTGCTTGAAGATATTAAGTTTGAATGATTTTGAATTTGATGAGG 6497
QY 1681 ACCTCCATGATATATCTACATGATGATTAACAAGTATGATCAAGGTTTCACT 1740
DB 6498 ACCTCCATGATATATCTACATGATGATTAACAAGTATGATCAAGGTTTCACT 6557
QY 1741 TTTTATGAGGCACTGAAAACATTTGCTATGATCAATAATGATATCATGATCAGGCTTGTG 1800
DB 6558 TTTTATGAGGCACTGAAAACATTTGCTATGATCAATAATGATATCATGATCAGGCTTGTG 6617
QY 1801 CTAAGAGTCTTATAGATGTTTCCCTATGATGCTTGTACAAATTTTACCTGATGAGATCAT 1860
DB 6618 CTAAGAGTCTTATAGATGTTTCCCTATGATGCTTGTGTCAAAATTTTACCTGATGAGATCAT 6677
QY 1861 AAGATTGGAAGTATATATTTATTTCTTTCTAGATTTGTTCTTTCTAGATGACA 1920
DB 6678 AAGATTGGAAGTATATATTTATTTCTTTCTAGATTTGTTCTTTCTAGATGACA 6737

2Y 1921 TTACTGGGAACATGAGCAATATTTGGATTGCTACTGATGTTGATGGCGTAGCTTAC 1980
 6738 TTACTGGGAACATGAGCAATATTTGGATTGCTACTGATGTTGATGGCGTAGCTTAC 6797
 2Y 1981 TTGATGCTGCTCAACGATCTAATTCATGAGCTTTATCTGATGCTATCCATTTGTGAA 2040
 6798 TTGATGCTGCTCAACGATCTAATTCATGAGCTTTATCTGATGCTATCCATTTGTGAA 6857
 2Y 2041 GATGTAAGTG 2050
 6858 GATGTAAGTG 6867

RESULT 2
 AF338431 11475 bp DNA linear PLN 27-MAR-2001
 LOCUS Aegilops tauschii starch branching enzyme I1a gene, complete cds.
 DEFINITION AF338431
 ACCESSION AF338431 GI:13447949
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Aegilops tauschii
 Aegilops tauschii
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Aegilops.
 1 (bases 1 to 11475)
 Rahman, S., Regina, A., Li, Z., Mukai, Y., Yamamoto, M.,
 Kosar-Hademi, B., Abrahams, S. and Morell, M.K.
 Comparison of starch-branching enzyme genes reveals evolutionary
 relationships among isoforms. Characterization of a gene for
 starch-branching enzyme I1a from the wheat genome donor Aegilops
 tauschii
 Plant Physiol. 125 (3), 1314-1324 (2001)

JOURNAL
 MEDLINE 21140316
 PUBMED 11244112
 2 (bases 1 to 11475)
 Rahman, S., Regina, A., Li, Z., Sharon, A. and Morell, M.K.
 Direct Submission
 Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Ross,
 Canberra, ACT 2601, Australia
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ACCESSION
AY235709.1 GI:30014041
VERSION
KEYWORDS
SOURCE
ORGANISM
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Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 691)
AUTHORS
White, S.R., Wilson, L.M., Tenailon, M.I., Gaut, B.S. and Buckler, E.S.
TITLE
Genetic diversity and selection in the maize starch pathway
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
MEDLINE
2247734
PUBMED
12244216
2 (bases 1 to 691)
REFERENCE
White, S.R., Wilson, L.M., Tenailon, M.I., Gaut, B.S. and Buckler, E.S.
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Direct Submission
Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
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D	139 TGCGCATCACTGGATGTGGGATTTCTCGCCTATTAACTATGGGAACTGGGAAAGTAC--G	196
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DEFINITION	Zea mays subsp. mays cultivar A272 amylose extender starch-branching enzyme (ael) gene, exons 12, 13, and 14 and partial cds.			
ACCESSION	AZ235690			
VERSION	AZ235690.1		GI:30014003	
KEYWORDS				
SOURCE				
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	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD			
	clade; Panicoidae; Andropogoneae; Zea.			
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REFERENCE	Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.			
TITLE	Genetic diversity and selection in the maize starch pathway			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)			
MEDLINE	22247734			
PUBMED	12244216			
REFERENCE	2 (bases 1 to 713)			
AUTHORS	Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.			
TITLE	IV.			
JOURNAL	Direct Submission			
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Matches 461; Conservative	0; Mismatches 192; Indels 55; Gaps 4;			
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Db 19 TTTGGTTTCATACCTTTTAACTTCTGCTTTTGTGTACTTGCAGTCAGCGCTCAAGTAAATAC 78

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RESULT 8

LOCUS AY235692 713 bp DNA linear PLN 16-Apr-2003

DEFINITION Zea mays subsp. mays cultivar B103 amylose extender starch-branching enzyme (ae1) gene, exons 12, 13, and 14 and partial cds.

ACCESSION AY235692

VERSION AY235692.1 GI:30014007

KEYWORDS

SOURCE Zea mays subsp. mays (maize)

ORGANISM Zea mays subsp. mays

REFERENCE 1 (bases 1 to 713) Tennison, M.I., Gaut, B.S. and Buckler, E.S. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)

REFERENCE 2 (bases 1 to 713) Whit, S.R., Wilson, L.M., Tennison, M.I., Gaut, B.S. and Buckler, E.S. Direct Submission Submitted (13-FEB-2003) Genetiscs, USDA-ARS, North Carolina State

FEATURES

source University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA

Location/Qualifiers

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Best Local Similarity 65.1%; Pred. No. 1.7e-40;
Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4;

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DEFINITION Zea mays subsp. mays cultivar B97 amylose extender starch-branching
ACCESSION AY235696
VERSION AY235696.1 GI:30014015
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 713)
AUTHORS White,S.R., Wilson,L.M., Tennilison,M.I., Gaut,B.S. and Buckler,E.S.
TITLE Genetic diversity and selection in the maize starch pathway
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
MEDLINE 22247734
PUBMED 12244216
REFERENCE
2 (bases 1 to 713)
White,S.R., Wilson,L.M., Tennilison,M.I., Gaut,B.S. and Buckler,E.S.
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IV.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State
University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
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Best Local Similarity 65.1%; Pred. No. 1.7e-40;
Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4;
QY 1343 TTCAGTTCATTCGCTTCATCAATGATTTTGTGTACCCCGACATCAATGCTCAATATATAC 1402
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QY 1403 CCTGACCGGTTTGAATGGTTTTCGATGCGACTGATACATTAATCTTCCACGCTGCTCAG 1462
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 1 (bases 1 to 713)
 AUTHORS Whit, S.R., Wilson, L.M., Tenailon, M.I., Gaut, B.S. and Buckler, E.S.
 TITLE Genetic diversity and selection in the maize starch pathway
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
 MEDLINE 22247734
 PUBMED 12244216
 REFERENCE 2 (bases 1 to 713)
 AUTHORS Whit, S.R., Wilson, L.M., Tenailon, M.I., Gaut, B.S. and Buckler, E.S.
 TITLE Direct Submission
 JOURNAL Submitted (13-FEB-2003) Genomics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
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ORIGIN

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 Best Local Similarity 65.1%; Pred. No. 1.7e-40;
 Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4;

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 ACCESSION AY235698.1 GI:30014019
 VERSION
 KEYWORDS
 SOURCE Zea mays subsp. mays (maize)
 ORGANISM Zea mays subsp. mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 713)
 AUTHORS Whit, S.R., Wilson, L.M., Tenailon, M.I., Gaut, B.S. and Buckler, E.S.
 TITLE Genetic diversity and selection in the maize starch pathway
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
 MEDLINE 22247734

PUBMED 12244216
2 (bases 1 to 713)
REFERENCE White,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State
University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
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Query 1403 CTTGACGGTTTGAATGGTTTGATGGACATGATACATTACTTCACGGTGGTCACG 1462
Db 79 TCTGGATGGTTGAATGGTTTGATGGATGATACATTAACATTACTTCACAGTGGTCACG 138
Query 1463 CGGCATATATGATGGATTTCTCGTATATCAACTATGGAGTTGGGAATAGTAG 1522
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Query 1583 GATATTCATTTCTTATGACGATTAAGATTTCTTACTGTCAACCGGAGATGGTGGCTTG 1642
Db 257 ACAATTTTATCCGATGACGATTTTAAGATTTCTTCTCCAAATGCTAAGTGGTGGCTG 316
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Query 2003 TTCATGACTTTATCCCTGATGCTGATTCATTCATTTGGAAGATGATAGTG 2050
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DEFINITION
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays subsp. mays (maize)
Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 713)
White,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
TITLE
AUTHORS
JOURNAL
MEDLINE
22247734
PUBMED
12244216
REFERENCE
2 (bases 1 to 713)
White,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State
University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
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exon
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Page 14

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Best Local Similarity 65.1%; Pred. No. 1.7e-40;  
Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4;  
  
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DB 19 TTTGGTTTCATACCTTTAACTTGTGCTTTTGTGTTACTTGCAGTCATGGGTCAAGTAATAC 78  
QY 1403 CCTTGAAGGTTGAATGTTGATGGCACTGATACACATTAATCTTCCACGGTGTCCACG 1462  
DB 79 TCTGATGGGTTGAATGTTTGTGATGATACAGATACACATTAATCTTCCACAGTGTCCACG 138  
QY 1463 CGGCCATCATGATGATGGGATTTCTGCTATTAATCACTATGGAGTGGGAAGTATGTAG 1522  
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QY 1523 CTCTGACTTCTGCACCATATTTGGCTAATGCTGTTCTGTATCTGTCTTACACATGTT 1582  
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DB 521 -----TGCATTTTACTTTAGTAACTTTTACGGGGAACTTCAATGAGT 563  
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 01:51:55 ; Search time 802.094 Seconds
(without alignments)
10857.595 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2025	98.8	11475	5	AAH78338 Nucleotid
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5	141	6.9	2726	5	AAH78337 Nucleotid
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9	122.8	6.0	3015	2	AAV05639 Rice gene
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15	110.6	5.4	2665	2	AAH69729 plasmid p
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20	105	5.1	2968	5	AAH78342 Nucleotid
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36	92.4	4.5	2975	2	AAH42635 Class A s
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38	91.8	4.5	2000	7	ADA72699 Rice gene
39	91.4	4.5	2000	7	ADA72630 Rice gene
40	91.2	4.4	2000	7	ADA72699 Rice gene
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ALIGNMENTS

RESULT 1
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AC AAX34650;
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DT 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
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DE Search branching enzyme II (SBE II) gene sequence.
XX
XX Search biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBS;
XX search branching enzyme; starch soluble synthase; debranching enzyme;
XX endosperm; wheat; barley; granule-bound synthase; glutenin; starch;
XX grain softness protein I; bacterial isomylase; glycogen synthase;
XX wBBE I-D4 gene; ss.
XX
XX Aegilops tauschii.
XX
XX PN WO9914314-A1.
XX
XX PD 25-MAR-1999.
XX
XX PF 11-SEP-1998; 98MO-AU000743.
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XX PR 12-SEP-1997; 97AU-00009108.
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XX PR 20-MAR-1998; 98AU-00002509.
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XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX (AUSU) UNIV AUSTRALIAN NAT.
XX (GOCOD) GOODMAN FIELDER LTD.
XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX
XX Li Z, Murrell M, Rahman S;
XX
XX WPI; 1999-229525/19.
XX
XX PT New isolated cereal plant enzyme genes used for, e.g. expression of
XX anticline sequences of granule bound synthase.
XX
XX PS Claim 8; Page 75-81; 17pp; English.
XX
XX CC The invention relates to a novel enzyme of starch biosynthetic pathway in
XX a cereal plant, where the enzyme is selected from starch branching enzyme
XX (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme

rice or maize. The methods and products can be used for targeting expression specifically to the endosperm of the seeds of cereal plants such as wheat or barley. They can be used for the expression of e.g. antisense sequences of granule-bound synthase (GBS), SBE II, low mol. wt. glutenin, grain softness protein I, bacterial isomylase, bacterial glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be used for modifying the characteristics of starch produced by a plant. The present sequence represents the SBE II gene sequence. (updated on 17-Oct-2003 to standardise OS field)

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Best Local Similarity 100.0%; Pred. No. 0;
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DB	4888	GGATACATGCACTGAGATATATGCAATCAGAGACATTCATATGCAAGCTTTGGG	4947
QY	121	TATTCACACATTCATTTTCTGTATACACTCTTACCCATTTGGAGCTATTACATCC	180
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DB	6508	ACCTTCATGATATATACATCAATGATATTAAGTAAAGTCAATCAAGTGGTTAGTAACT	6567
QY	1741	TTTTTAGGGAAGTGAACATTTGCTATGATATTAACATGATATATGATGATGATGATG	1800
DB	6568	TTTTTAGGGAAGTGAACATTTGCTATGATATTAACATGATATATGATGATGATGATG	6627
QY	1801	CTACGAGTCTTATAGTATGCTTCCCTATGATGCTTGAATTTTAACTGATGATGATG	1860
DB	6628	CTACGAGTCTTATAGTATGCTTCCCTATGATGCTTGAATTTTAACTGATGATGATG	6687
QY	1861	AAGATTGGAAGTATATATTTATTTCTTTCTAGATTTGTTCTGTTCTGATGATGATG	1920
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QY 2041 GATGTAAGTG 2050
Db 6868 GATGTAAGTG 6877

RESULT 2
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AC AAH78338;
XX
DT 26-NOV-2001 (first entry)
XX

DE Nucleotide sequence of a starch branching enzyme designated F2.
XX
XX Wheat; starch branching enzyme; BE1b; SBE; transgenic plant;
KM starch biosynthetic pathway; amylopectin; F2; amylose; ss.
XX
XX Aegilops tauschii.
XX
XX MO200162934-A1.
XX
XX 30-AUG-2001.
XX

PF 21-FEB-2001; 2001MO-AUD000175.
XX
XX 21-FEB-2000; 2000AU-00005742.
XX

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (GOOD-) GOODMAN FIELDER LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX

XX Morell M, Rahman S;
XX WPI; 2001-570635/64.
XX
XX Nucleic acids encoding wheat starch branching enzyme 1b, useful for
PT altering the amylose and amylopectin content of cereal plants, e.g. wheat
PT and barley.
XX
XX
XX Example 1; Fig 2; 103pp; English.

XX The present sequence encodes a wheat starch branching enzyme of Aegilops
CC tauschii, designated F2. A. tauschii is likely to be the ancestral D
CC genome donor of wheat. Probes isolated from the present sequence were
CC used to identify type II starch branching enzymes (SBEs) in wheat,
CC especially BE1b. The BE1b nucleic acids may be used to genetically
CC transform cereal plants such as wheat or barley and for altering their
CC nutritional content by modulating the starch biosynthetic pathway to vary
CC levels of amylopectin and/or amylose produced in the plant
XX

XX Sequence 11475 BP; 3093 A; 2259 C; 2423 G; 3689 T; 0 U; 11 Other;
XX
XX Query Match 98.8%; Score 2025; DB 5; Length 11475;
XX Best Local Similarity 99.8%; Pred. No. 0; Mismatches 1; Indels 4; Gaps 2;
XX Matches 2049; Conservative 0; Mismatches 1; Indels 4; Gaps 2;

QY 1 CCGAAGATAAATTCATATGCTAATTTTGGATGAGGTGTCGCAAGATTAAAGGCTT 60
Db 4821 CCGAAGATAAATTCATATGCTAATTTTGGATGAGGTGTCGCAAGATTAAAGGCTT 4880
QY 61 GGATACATGAGTGCAGATATATGCAATCCAGAGCATTCATATATGCAAGCTTTGGG 120
Db 4881 GGATACATGAGTGCAGATATATGCAATCCAGAGCATTCATATATGCAAGCTTTGGG 4940
QY 121 TATTACACATCCATTTTCTTGTATAGAC-TCTTACCCATTGGAGCATATAGATC 179

Db 4941 TATTACACATCCATTTTCTTGTATAGACANTCTCACCCATTGGAGCATATAGATC 5000
QY 180 CTATGCTTCATGACATAAATATTTGGATATATATCTTTATATAGATATATAGTACAC 239
Db 5001 CTATGCTTCATGACATAAATATTTGGATATATATCTTTATATAGATATATAGTACAC 5060
QY 240 TACACTTATGATCTG--AAAAAGATCTTTATGTTGTGGCTGTCCAGGTACCA 296
Db 5061 TACACTTATGATCTG--AAAAAGATCTTTATGTTGTGGCTGTCCAGGTACCA 5120
QY 297 TGTACTAATTTTGTGACCAAGTAGCCGTTTGGAACTCCAGAGATTAAATCCCTT 356
Db 5121 TGTACTAATTTTGTGACCAAGTAGCCGTTTGGAACTCCAGAGATTAAATCCCTT 5180
QY 357 GATGATAGAGCATAGAGCTTGCTTGTCTTATGATATGTTCTATAGTAAAT 416
Db 5181 GATGATAGAGCATAGAGCTTGCTTGTCTTATGATATGTTCTATAGTAAAT 5240
QY 417 AGTCCAAATTAATTTAGCTGTTTACTGTTTATCTGATCTTAAGGAAATCCAGGC 476
Db 5241 AGTCCAAATTAATTTAGCTGTTTACTGTTTATCTGATCTTAAGGAAATCCAGGC 5300
QY 477 AATTATGATCATTTGTCAAAAGCTAAGAGTGGCAAGTGAATGTCAAAATCTAGAGTG 536
Db 5301 AATTATGATCATTTGTCAAAAGCTAAGAGTGGCAAGTGAATGTCAAAATCTAGAGTG 5360
QY 537 GCATTAAGAAAATTGGCAAAAATCTAGAGTGGCAAAAATTAATTTTCCATCTTAATGG 596
Db 5361 GCATTAAGAAAATTGGCAAAAATCTAGAGTGGCAAAAATTAATTTTCCATCTTAATGG 5420
QY 597 CAGGGCCCTATGGCCGAATATTTTCCATCTTAATTTGCTATAGTGGTACTGCTTCTTTT 656
Db 5421 CAGGGCCCTATGGCCGAATATTTTCCATCTTAATTTGCTATAGTGGTACTGCTTCTTTT 5480
QY 657 TCTCAGATGATTAATAACAGATGGAACATGAATGATTTGGTACATGATTAATCTGACA 716
Db 5481 TCTCAGATGATTAATAACAGATGGAACATGAATGATTTGGTACATGATTAATCTGACA 5540
QY 717 GTTCCATAGAAATTCGTTTGTATATGGAACAACATTTGATGCCATAGATGTGATGAG 776
Db 5541 GTTCCATAGAAATTCGTTTGTATATGGAACAACATTTGATGCCATAGATGTGATGAG 5600
QY 777 AATTCAGATGATTAATAACAGATGGAACATGAATGATTTGGTACATGATTAATCTGACA 836
Db 5601 AATTCAGATGATTAATAACAGATGGAACATGAATGATTTGGTACATGATTAATCTGACA 5660
QY 837 GTTGCAGATGGAATACTGACAGCAATACCTCACTGATAGTGGCCAGGCCCATTTGC 896
Db 5661 GTTGCAGATGGAATACTGACAGCAATACCTCACTGATAGTGGCCAGGCCCATTTGC 5720
QY 897 CAGCTTCATATGATGATTTCTCCCTGTTGAATTCATTTGAACATATTTACTTAAGTTC 956
Db 5721 CAGCTTCATATGATGATTTCTCCCTGTTGAATTCATTTGAACATATTTACTTAAGTTC 5780
QY 957 TTTGATTTGCTTAAGTCAACCTTTTAATTTGACCAAGCTATTTGGAATTAATATGAA 1016
Db 5781 TTTGATTTGCTTAAGTCAACCTTTTAATTTGACCAAGCTATTTGGAATTAATATGAA 5840
QY 1017 CATCTCAACACCAAAATTTACTTTGATCAGATTAACAATTTTATTTATTTATATAGCAC 1076
Db 5841 CATCTCAACACCAAAATTTACTTTGATCAGATTAACAATTTTATTTATTTATATAGCAC 5900
QY 1077 ATCTTGTATGTTTGAATATCAGACATTTTCTTATAGACTTGGTCAATATAGAGAGT 1136
Db 5901 ATCTTGTATGTTTGAATATCAGACATTTTCTTATAGACTTGGTCAATATAGAGAGT 5960
QY 1137 TTGACTTAGAGCAAACTTGAACCTTCAATCAATTTTGGATCAGAGGAAATCAATATATATA 1196
Db 5961 TTGACTTAGAGCAAACTTGAACCTTCAATCAATTTTGGATCAGAGGAAATCAATATATATA 6020
QY 1197 TAGATAGATGTCACACTTCAACAAAATTCAGACCTTGTACACATATATGATCAGAC 1256

QY	1257	CATCTGTTTGGCTTTAGCCACCTGCTTCATATTATTTANGTGTGGACCTAAATCTACTTTTC	1316	FT	Key	Location/Qualifiers
DB	6081	CATCTGTTTGGCTTTAGCCACCTGCTTCATATTATTTATGTTTGTACCTAAATCTACTTTTC	6140	FT	misc_signal	597..602
QY	1317	CTTCTTACTGGTTTGGTTGATTTCTATTTCAGTTGCATTTGCTTCATCAATGATTTTGTGTA	1376	FT	repeat_unit	/*tag= a /note= "I box, conserved in RBCs genes"
DB	6141	CTTCTTACTGGTTTGGTTGATTTCTATTTCAGTTGCATTTGCTTCATCAATGATTTTGTGTA	6200	FT	misc_signal	1475..1481
QY	1377	CCCTGAGATCATTCGCAATAATACCCTTGACGGTGTGAATGGTTTCGATGGCAGCTGAT	1436	FT	misc_signal	/*tag= b /note= "RY repeat, distal regulatory element"
DB	6201	CCCTGAGATCATTCGCAATAATACCCTTGACGGTGTGAATGGTTTCGATGGCAGCTGAT	6260	FT	misc_signal	1967..1973
QY	1437	ACACATTACTTCCACGAGTGTGTCACGCGGCATCATTTGATGGGATTCGTCTATTC	1496	FT	GC_signal	/*tag= c /note= "Hex, conserved element found in plant histone gene promoters"
DB	6261	ACACATTACTTCCACGAGTGTGTCACGCGGCATCATTTGATGGGATTCGTCTATTC	6320	FT	GC_signal	2593..2599
QY	1497	AACATAGGAGTTGGGAAGATATGATGCTCTGACTTCTGTCAACCATTTTGGCTAACTGTT	1556	FT	GC_signal	/*tag= d /note= "MRE box, motif essential for metal ion-dependent induction of metallothionein genes"
DB	6321	AACATAGGAGTTGGGAAGATATGATGCTCTGACTTCTGTCAACCATTTTGGCTAACTGTT	6380	FT	GC_signal	2666..2671
QY	1557	CCGTAAATCTGTTCTTACACATGTTGATATTCATTCCTATTCGAGGATTTGAGATTTCTT	1616	FT	misc_signal	/*tag= e 2738..2743
DB	6381	CCGTAAATCTGTTCTTACACATGTTGATATTCATTCCTATTCGAGGATTTGAGATTTCTT	6440	FT	GC_signal	/*tag= f 2831..2836
QY	1617	ACTGTCAAAACGCGAGATGTGTGCTTGAAGAATAATAGTTGATGATTTTCATTTGATGG	1676	FT	GC_signal	/*tag= g 2838..2844
DB	6441	ACTGTCAAAACGCGAGATGTGTGCTTGAAGAATAATAGTTGATGATTTTCATTTGATGG	6500	FT	TATA_signal	/*tag= h /note= "MRE box, motif essential for metal ion-dependent induction of metallothionein genes"
QY	1677	GGTGACCTCCATGATGATTAATCAATCATGATTAACAAGTAAATGATCAAGTGTTCAGT	1736	FT	exon	2874..2879
DB	6501	GGTGACCTCCATGATGATTAATCAATCATGATTAACAAGTAAATGATCAAGTGTTCAGT	6560	FT	exon	2933..2936
QY	1737	AACATTTTAAAGGACATGGAACAATTCCTATGATCATCAATGATGATCATGAGACT	1796	FT	CDS	/*tag= i 2965..3176
DB	6561	AACATTTTAAAGGACATGGAACAATTCCTATGATCATCAATGATGATCATGAGACT	6620	FT	intron	/*tag= j /number= 1
QY	1797	TGTGTACGAGAGTCTTATGATGATTCCTATGATGCTTGTACAAATTTTACCTGATGAGATC	1856	FT	exon	/*tag= k /note= "contains introns"
DB	6621	TGTGTACGAGAGTCTTATGATGATTCCTATGATGCTTGTACAAATTTTACCTGATGAGATC	6680	FT	intron	/*tag= l /number= 1
QY	1857	ATGGAAGATTGGAAGTATTAATTTATTTCTTTCTAAGTTGTTCTTCTGTCTAGAT	1916	FT	intron	/*tag= m /number= 1
DB	6681	ATGGAAGATTGGAAGTATTAATTTATTTCTTTCTAAGTTGTTCTTCTGTCTAGAT	6740	FT	exon	/*tag= n /number= 2
QY	1917	GACATTTACGGGAGACATAGCGCAATTTTGGATTGCTGATGTTGATGGCGTAGT	1976	FT	intron	/*tag= o /number= 2
DB	6741	GACATTTACGGGAGACATAGCGCAATTTTGGATTGCTGATGTTGATGGCGTAGT	6800	FT	intron	/*tag= p /number= 3
QY	1977	TTACTTGATGCTGCTCAACGATCTAATTCATGAGCTTATATCTGATGCTGATCCATTGG	2036	FT	exon	/*tag= q /number= 3
DB	6801	TTACTTGATGCTGCTCAACGATCTAATTCATGAGCTTATATCTGATGCTGATCCATTGG	6860	FT	intron	/*tag= r /number= 4
QY	2037	TGAAGATGTAAGTG	2050	FT	intron	/*tag= s /number= 4
DB	6861	TGAAGATGTAAGTG	6874	FT	exon	/*tag= t /number= 5
RESULT 3	AAZ35393	standard; DNA; 23449 BP.		FT	intron	/*tag= u /number= 5
ID	AAZ35393			FT	exon	/*tag= v /number= 5
XX	AAZ35393;			FT	exon	/*tag= w /number= 6
XX	27-MAR-2000	(first entry)		FT	intron	/*tag= x /number= 7
DE	Maize	amylose-extender (Ae) gene encoding starch branching enzyme.		FT	intron	/*tag= y
XX	Starch	branching enzyme IIb; amylose-extender gene; Ae gene; maize; corn;		FT	exon	
KM	promoter;	expression control element; endosperm; transgenic plant; ss.		FT	intron	
OS	Zea	mays.		FT	intron	
XX				FT	intron	

[illegible]

XX 21-FEB-2000; 2000AU-00005742.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX (GOOD-) GOODMAN FIELDER LTD.
 XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
 XX Morell M, Rahman S;
 XX WPI; 2001-570635/64.
 XX
 XX Nucleic acids encoding wheat starch branching enzyme IIb, useful for
 PT altering the amylose and amylopectin content of cereal plants, e.g. wheat
 PT and barley.
 XX
 XX Example 1; Fig 1; 103pp; English.
 XX
 XX The present sequence encodes wheat starch branching enzyme 9, designated
 CC BEIIa. The specification describes BEIIb. BEIIb is a type II starch
 CC branching enzyme (SBE). The BEIIb nucleic acids may be used to
 CC genetically transform cereal plants such as wheat or barley and for
 CC altering their nutritional content by modulating the starch biosynthetic
 CC pathway to vary levels of amylopectin and/or amylose produced in the
 CC plant
 XX
 XX Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 6.9%; Score 141; DB 5; Length 2726;
 Best Local Similarity 72.2%; Pred. No. 1.3e-22;
 Matches 242; Conservative 0; Mismatches 5; Indels 88; Gaps 1;
 XX
 QY 1383 AGTATTCGTCTAAATTAATACCTTGACGGTTGATGGTTGATGGACGATACACT 1442
 DB 1168 AGTATTCATCAATAATTAATACCTTGACGGTTGATGGACGATACACT 1227
 QY 1443 TACTTCACGGTGTGTCACGCGCCATCATTTGATGGATTCCTGCTATTCACATAT 1502
 DB 1228 TACTTCACGGTGTGTCACGCGCCATCATTTGATGGATTCCTGCTATTCACATAT 1287
 QY 1503 GGGAGTTGGAGGATGATGCTGACTCTGTCTACCAATTTGGCTAACTGTTCTCTGT 1562
 DB 1288 GGGAGTTGGAGGATGATGCTGACTCTGTCTACCAATTTGGCTAACTGTTCTCTGT 1300
 QY 1563 AATCTGTTCTTACACATGTTGATATTTCTTATGACGATTTGAGTTCTTACTGTC 1622
 DB 1301 -----TATTGAGATTTCTTACTGTC 1319
 QY 1623 AAAGCGAGATGATGCTTGAAGATATATAGTTGATGGATTTGATGGAGGTGAC 1682
 DB 1320 AAAGCGAGATGATGCTTGAAGATATATAGTTGATGGATTTGATGGAGGTGAC 1379
 QY 1683 CTCGATGATGATTAATCAACATGATTAACAAGTAA 1717
 DB 1380 CTCGATGATGATTAATCAACATGATTAACAAGTAA 1414
 XX
 XX RESULT 6
 AAAX34650/c
 ID AAAX34650 standard; DNA; 11473 BP.
 XX
 AC AAAX34650;
 XX
 XX 17-OCT-2003 (revised)
 DT 05-JUL-1999 (first entry)
 XX
 XX Starch branching enzyme II (SBE II) gene sequence.
 DE
 XX Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBS5;
 KM starch branching enzyme; starch soluble synthase; debranching enzyme;
 KM endosperm; wheat; barley; granule-bound synthase; glutenin; starch;
 KM grain softness protein I; bacterial isoamylase; glycogen synthase;
 KM WSBE I-D4 gene; ss.
 XX

OS Aegilops tauschii.
 XX
 XX MO9914314-A1.
 XX
 XX 25-MAR-1999.
 XX
 XX
 XX 11-SEP-1998; 98MO-AU000743.
 XX
 XX 12-SEP-1997; 97AU-00009108.
 XX 20-MAR-1998; 98AU-00002509.
 XX
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX (AUSU) UNIV AUSTRALIAN NAT.
 XX (GOOD-) GOODMAN FIELDER LTD.
 XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
 XX
 XX Li Z, Morell M, Rahman S;
 XX
 XX WPI; 1999-229525/19.
 XX
 XX
 XX Claim 8; Page 75-81; 171pp; English.
 XX
 XX The invention relates to a novel enzyme of starch biosynthetic pathway in
 CC a cereal plant, where the enzyme is selected from starch branching enzyme
 CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme
 CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of
 CC rice or maize. The methods and products can be used for targeting
 CC expression specifically to the endosperm of the seeds of cereal plants
 CC such as wheat or barley. They can be used for the expression of e.g.
 CC antisense sequences of granule-bound synthase (GBS), SBE II, low mol.
 CC wt. glutenin, grain softness protein I, bacterial isoamylase, bacterial
 CC glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be
 CC used for modifying the characteristics of starch produced by a plant. The
 CC present sequence represents the SBE II gene sequence. (Updated on 17-OCT-
 CC 2003 to standardise OS field)
 XX
 XX Sequence 11473 BP; 3096 A; 2263 C; 2423 G; 3691 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 6.2%; Score 126.2; DB 2; Length 11473;
 Best Local Similarity 64.6%; Pred. No. 5.2e-19;
 Matches 188; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
 XX
 QY 911 ATGTTACTTCCTCGTTGAATTCATTTGAACATATTACTTAAGTTCTTCAATTTGGCTTAA 970
 DB 6028 ATCTAATATTATTGATGTTCCCTCTGATCCAAATTTGATGAAGTCTGATTTGCTCAA 5969
 QY 971 GTCAACTCTTTTAAGTTGACCAAGCTATTGGAATAATATATCAACATCTACACACCA 1030
 DB 5968 GTCAACTCTCTTAATTTTGCACAGCTATAGAAAAATGCTGATATCTACACACATCA 5909
 QY 1031 AATTACTTGTATGATTAACAATTTTATTTATTTATATTATTAAGACATCTTTGATGTGT 1090
 DB 5908 AAGATGCTAATATATATAAATAAATGTTATCTGATCAAGTATTTGGTGTGT 5849
 QY 1091 AGATATCAGACATTTTTCATATAGACTTGTCTAAATATAGAGACTTGACTTAGACCA 1150
 DB 5848 AGATGTTGATATATTTTCCAAATAGACTTGTCAAAAGTTGAAGTTGACTTAGACCA 5789
 QY 1151 ATCTAGAACTTCATCAATTTGATTCAGAGGAACATCAATAATATATGAT 1201
 DB 5788 ATGAGAACTTTTATGATATATGTTTCAATATGATTAATTCACAGGAGTAACT 5738
 XX
 XX RESULT 7
 AAH78338/c
 ID AAH78338 standard; cDNA; 11475 BP.
 XX
 XX AAH78338;
 AC
 XX
 XX 26-NOV-2001 (first entry)
 DT

XX DE Nucleotide sequence of a starch branching enzyme designated F2.
XX KW wheat; starch branching enzyme; BE1b; SB2; transgenic plant;
XX KM starch biosynthetic pathway; amylopectin; F2; amylose; ss.
XX OS Aegilops tauschii.
XX PN WO200162934-A1.
XX PD 30-AUG-2001.
XX PF 21-FEB-2001; 2001MO-AU000175.
XX PR 21-FEB-2000; 2000AU-00005742.
XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PA (GOOD-) GOODMAN FIELDER LTD.
XX PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX PI Morell W, Rahman S;
XX PI WPI; 2001-570635/64.
XX PT Nucleic acids encoding wheat starch branching enzyme IIB, useful for
XX PT altering the amylose and amylopectin content of cereal plants, e.g. wheat
XX PT and barley.
XX PS Example 1; Fig 2; 103pp; English.
XX CC The present sequence encodes a wheat starch branching enzyme of Aegilops
XX CC tauschii, designated F2. A. tauschii is likely to be the ancestral D
XX CC genome donor of wheat. Probes isolated from the present sequence were
XX CC used to identify type II starch branching enzymes (SBEs) in wheat,
XX CC especially BE1b. The BE1b nucleic acids may be used to genetically
XX CC transform cereal plants such as wheat or barley and for altering their
XX CC nutritional content by modulating the starch biosynthetic pathway to vary
XX CC levels of amylopectin and/or amylose produced in the plant
XX SQ Sequence 11475 BP; 3093 A; 2259 C; 2423 G; 3689 T; 0 U; 11 Other;
XX SQ
XX Query Match 6.2%; Score 126.2; DB 5; Length 11475;
XX Best Local Similarity 64.6%; Pred. No. 5.2e-19;
XX Matches 188; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 911 AAGTACTTCCCTGGTGAATTCATTGAACATATTAATTAAGTTCTTCATTGCTCTAA 970
DB 6025 ATCTATATTAATTTGATGTCCTCCCTGATCCAAATGATGAAGTTCTGATTTGCTTAA 5966
QY 971 GTAAACTTTCTTAAGTTGACCAAGTCTATGSAATAATATCAACTTCAACAACCA 1030
DB 5965 GTCAAACTTCTATATATTGACCAAGTCTATGSAATAATGCTGATATCAACAACCA 5906
QY 1031 AATTAATTTGATGATCAATTAACATTTTATTTATTTATTAAGACATCTTGAATGTTGT 1090
DB 5905 AAGATGTCCTAATTAATTAATAAATTTATCTGATCAAGTAAATTTGGTGTGT 5846
QY 1091 AGATATCAGACATTTTCTATAGACTTGTCAAAATATAGAAAGTTTGAAGTAAAGCA 1150
DB 5845 AGATGTCCTAATTTTCCATATAGACTTGTCAAAAGTTTGAAGTAAAGTAAAGCA 5786
QY 1151 ATCTAGACTTCAATCAATTTGATCGAGGAAACATTAATATATGAT 1201
DB 5785 ATGAAGACTTTAAGTAAATATGTTCAATGATTTCAAGGAAAGTAAACAT 5735

XX DE Rice DNA sequence Seq ID523 related to grain filling.
XX KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
XX KM carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
XX KM tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
XX KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
XX KW gene; ds; plant.
XX OS Oryza sativa.
XX PN WO2003000905-A2.
XX PD 03-JAN-2003.
XX PF 21-JUN-2002; 2002MO-IB002450.
XX PR 22-JUN-2001; 2001US-0300112P.
XX PR 26-SEP-2001; 2001US-0325277P.
XX PR 20-DEC-2001; 2001US-0342327P.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
XX PI Glazebrook J, Katagiri F, Kreps J, Provart N, Rieke D;
XX DR WPI; 2003-229341/22.
XX DR P-PsDB; ADC08218.
XX PT New plant genes encoding polypeptides having an activity involved in or
XX PT associated with the synthesis, metabolism or degradation of carbohydrates
XX PT in the plant grain useful in generating plants having improved
XX PT nutritional properties.
XX PS Claim 35; SEQ ID NO 523; 130pp; English.
XX CC This invention, in the area of plant biotechnology, relates to novel
XX CC polynucleotides comprising a nucleotide sequence encoding a protein which
XX CC is involved in or associated with the synthesis, metabolism or
XX CC degradation of carbohydrates in the plant grain and the expression of
XX CC which is up-regulated during grain filling. The plant is selected from
XX CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
XX CC sugarbeet, wheat, and rice. The invention may be useful for the
XX CC improvement of protein, oil, starch, fibre and moisture content of the
XX CC cereal grains. In addition, carbohydrate levels may be modified to a more
XX CC desirable level using the present invention. The present sequence is a
XX CC DNA sequence encoding a rice protein of the invention. Note: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/publishedpct_sequences.
XX SQ Sequence 2304 BP; 610 A; 457 C; 620 G; 617 T; 0 U; 0 Other;
XX SQ
XX Query Match 6.0%; Score 122.8; DB 9; Length 2304;
XX Best Local Similarity 91.5%; Pred. No. 2e-18;
XX Matches 130; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1909 TTCTAGATGACATTTTACTGGAACCTATGCGAATATTTTGGATTTGCTACTGATGTTGAT 1968
DB 1354 TTACAGTGCGACATTTTACTGGAACCTATGCGAATATTTTGGATTTGCTACTGATGTTGAT 1413
QY 1968 GCGGAGTTTACTGATGCTGTCACAGATCTAATTCATGAGCACTTATCCGTGAGCTGTA 2028
DB 1414 GCGAGAGTTTACTGATGCTGTCACAGATCTAATTCATGAGCACTTATCCGTGAGCTGTA 1473
QY 2029 TCCATTGTTGAAGATGTAAGTG 2050
DB 1474 GCCATTGTTGAAGATGTCAGCG 1495

RESULT 9
ID ADA71289 standard; DNA; 2655 BP.
XX 18-DEC-2003 (first entry)

XX AD71289;
AC Rice, type IV starch branching enzyme; amylopectin synthesis; ds.
XX 20-NOV-2003 (first entry)
XX
XX Rice gene, SEQ ID 4612.
DE
XX Plant, bacterial infection; fungal infection; viral infection; rice;
KM gene; ds.
XX
XX Oryza sativa.
OS
XX WO2003000898-A1.
PN
XX 03-JAN-2003.
PD
XX 22-JUN-2001; 2001WO-IB001105.
PF
XX 22-JUN-2001; 2001WO-IB001105.
PR
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
PA
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX Katagiri F, Qian S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
DR
XX Identifying at least one gene involved in plant resistance or response to
XX pathogenic infection for conferring resistance or tolerance to a plant to
XX bacterial, fungal or viral infection by determining or detecting plant
XX gene expression.
PT
XX
PS Claim 6; SEQ ID NO 4612; 8999P; English.
XX
XX The present invention relates to a method (M1) for identifying genes
XX involved in plant resistance or response to pathogenic infection. M1
XX comprises identifying a gene whose expression is significantly altered in
XX the incompatible interaction of plant gene expression relative to
XX expression of the gene in an uninfected plant, in a mutant plant that
XX does not express a gene associated with response to pathogenic infection,
XX or in a corresponding incompatible or compatible interaction. (M1) is
XX useful for conferring resistance to resistance or tolerance to a plant to
XX bacterial, fungal or viral infection. The present sequence was used to
XX illustrate the invention.
XX
XX Sequence 2655 BP; 714 A; 529 C; 680 G; 732 T; 0 U; 0 Other;
SQ
XX
XX Query Match 6.0%; Score 122.8; DB 7; Length 2655;
XX Best Local Similarity 91.5%; Pred. No. 2.1e-18;
XX Matches 130; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX 1909 TTCTAGATGACATTACTGGAACATATGCGAATATTTGGATTGCTACTGATGTTGAT 1968
XX |||||
XX 1573 TTACAGGAGGACATTACTGCGAATATGCGAATATTTGGATTGCTACTGATGTTGAT 1632
XX |||||
XX 1969 GCGGTAGTTTACTGATGCTGCTCAAGATCTTAATTCATGACTTTATCTGATGCTGA 2028
XX |||||
XX 1633 GCACTAGTTTACTGATGCTGCTCAAGATCTTAATTCATGACTTTATCTGATGCTGA 1692
XX |||||
XX 2029 TCCATTGGTGAAGATGTAAGTG 2050
XX |||||
XX 1693 GCCATTGGTGAAGATGTCAGCG 1714
XX |||||
XX
XX RESULT 10
XX ID AAV05639 standard; cDNA to mRNA; 3015 BP.
XX AAV05639;
AC
XX 25-MAR-2003 (revised)
DT 01-MAY-1998 (first entry)
XX

DE Rice type IV starch branching enzyme cDNA.
XX
XX Rice; type IV starch branching enzyme; amylopectin synthesis; ds.
XX
XX Oryza sativa.
OS
XX
XX Key Location/Qualifiers
FH 129..2654
FT CDS /*tag= a
FT sig_peptide 129..287
FT /*tag= b
FT mat_peptide 288..2651
FT /*tag= c
FT /*product= "type_IV_starch_branching_enzyme"
XX
XX JP10004970-A.
PN
XX 13-JAN-1998.
PD
XX 24-JUN-1996; 96JP-00162983.
PF
XX 24-JUN-1996; 96JP-00162983.
PR
XX 24-JUN-1996; 96JP-00162983.
PS
XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
PA (MITK) MITSUI TOATSU CHEM INC.
XX
XX WPI; 1998-133625/13.
DR P-PSDB; AAW41763.
XX
XX Rice starch branching enzyme gene - synthesises amylopectin to yield high
XX quality starch.
PT
XX
PS Claim 4; Page 5-8; 13pp; Japanese.
XX
XX The present sequence encodes the rice type IV starch branching enzyme,
XX which has the ability to synthesise amylopectin. The quality of starch is
XX improved by the use of the protein. (Updated on 25-MAR-2003 to correct PA
XX field.)
XX
XX Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 U; 0 Other;
SQ
XX
XX Query Match 6.0%; Score 122.8; DB 2; Length 3015;
XX Best Local Similarity 91.5%; Pred. No. 2.2e-18;
XX Matches 130; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX 1909 TTCTAGATGACATTACTGGAACATATGCGAATATTTGGATTGCTACTGATGTTGAT 1968
XX |||||
XX 1626 TTACAGGAGGACATTACTGCGAATATGCGAATATTTGGATTGCTACTGATGTTGAT 1685
XX |||||
XX 1969 GCGGTAGTTTACTGATGCTGCTCAAGATCTTAATTCATGACTTTATCTGATGCTGA 2028
XX |||||
XX 1686 GCGGTAGTTTACTGATGCTGCTCAAGATCTTAATTCATGACTTTATCTGATGCTGA 1745
XX |||||
XX 2029 TCCATTGGTGAAGATGTAAGTG 2050
XX |||||
XX 1746 GCCATTGGTGAAGATGTCAGCG 1767
XX |||||
XX
XX RESULT 11
XX ID ADC07807 standard; DNA; 2307 BP.
XX ADC07807;
AC
XX 18-DEC-2003 (first entry)
DT
XX
XX Rice DNA sequence Seq ID73 related to grain filling.
DE
XX Plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
XX carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
XX tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarcane;
XX wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
XX gene; ds. plant

XX Oryza sativa.
OS
XX
PN MO2003000905-A2.
XX
XX 03-JAN-2003.
XX
PF 21-JUN-2002; 2002MO-IB002450.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 26-SEP-2001; 2001US-0325277P.
PR 20-DEC-2001; 2001US-0342327P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Glazebrook U, Katagiri F, Kreps U, Provart N, Ricke D;
DR MPI; 2003-229341/22.
XX P-PSDB; ADC07808.
XX
PT New plant genes encoding polypeptides having an activity involved in or
PT associated with the synthesis, metabolism or degradation of carbohydrates
PT in the plant grain useful in generating plants having improved
PT nutritional properties.
PS Claim 2; SEQ ID NO 73; 130pp; English.
XX
CC This invention, in the area of plant biotechnology, relates to novel
CC polynucleotides comprising a nucleotide sequence encoding a protein which
CC is involved in or associated with the synthesis, metabolism or
CC degradation of carbohydrates in the plant grain and the expression of
CC which is up-regulated during grain filling. The plant is selected from
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
CC sugarcane, wheat, and rice. The invention may be useful for the
CC improvement of protein, oil, starch, fibre and moisture content of the
CC cereal grains. In addition, carbohydrate levels may be modified to a more
CC desirable level using the present invention. The present sequence is a
CC DNA sequence encoding a rice protein of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/publishedpc_sequences.
XX
XX Sequence 2307 BP; 608 A; 465 C; 620 G; 614 T; 0 U; 0 Other;
SQ
Query Match 5.8%; Score 119.2; DB 9; Length 2307;
Best Local Similarity 85.3%; Pred. No. 1.4e-17;
Matches 133; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1895 AAGTTGTTCTTCTGTCTAGATGACATTGAGGAACTATGCGAATATTTGGATTG 1954
DB 1279 ATGTATCTCATCTATGTTTACAGCATTTACTGGAATATGCGAATATTTGGATTG 1338
QY 1955 CTACTGATGTTGATGCGGTAATTTACTGATGCTGCTGCAAGATCTAATTCATGGAATT 2014
DB 1339 CTACTGATGTTGATGCGGTAATTTACTGATGCTGCTGCAAGATCTAATTCATGGAATT 1398
QY 2015 ATCCTGATGCTGATTCATTTGATGCTGGAAGATGTAAGT 2050
DB 1399 ATCCTGAGGCTGATGCGCATTTGTTGTAAGATGTCAGCG 1434
RESULT 12
AAT69737
ID AAT69737 standard; DNA; 2087 BP.
XX
XX AAT69737;
XX
XX 10-SEP-1997 (first entry)
XX
XX Corn starch branching enzyme IIb gene fragment in pBB96.
XX
XX Starch branching enzyme IIb; SBEIIb; corn; maize; antisense; amylopectin;

KM transgenic plant; pBB96; ss.
XX
XX Zea mays.
OS
XX
PN MO9722703-A2.
XX
XX 26-JUN-1997.
XX
XX 12-DEC-1996; 96WO-US019678.
XX
XX 20-DEC-1995; 95US-0009113P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Hubbard NL, Klein TM, Broglie KE;
PI MPI; 1997-341694/31.
XX
XX Transgenic corn in which grain derived starch fine structure is
XX controlled - specifically branch chain distribution of amylopectin,
XX useful in preparation of thickened foodstuff.
XX
XX Example 4; Page 56-57; 92pp; English.
XX
XX A cDNA insert (AAT69737) in plasmid pBB96 comprises a 2.09 kb fragment of
XX corn starch branching enzyme IIb (SBEIIb) cDNA (see also AAT69729),
XX starting at the initiating ATG codon of the coding region and terminating
XX 312 bp 5' of the translation termination codon. It was obtained by site-
XX specific mutagenesis of the SBEIIb gene in plasmid pBB240 to generate an
XX NcoI site at the ATG start site, and EcoRI digestion of the mutagenised
XX plasmid. The 2.09 kb fragment was inserted, in sense orientation, between
XX the zein promoter and 3' regions in vector pML103 to produce pBB96. Co-
XX suppression and antisense techniques can be used to inhibit SBEIIb in
XX transgenic plants and thereby alter starch properties
SQ
Sequence 2087 BP; 565 A; 396 C; 553 G; 573 T; 0 U; 0 Other;
SQ
Query Match 5.4%; Score 110.6; DB 2; Length 2087;
Best Local Similarity 79.4%; Pred. No. 1.3e-15;
Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1383 AGTCATTCGTCGAATATATCCCTTGACGGTTGAAATGTTTCGATGCACTGATACAT 1442
DB 1138 AGTCATTCGTCGAATATATCCCTTGACGGTTGAAATGTTTCGATGCACTGATACAT 1197
QY 1443 TACTTCACAGTGTGTCACGCGGCATTCATTTGATGCGGATTCCTGCTATTCACATAT 1502
DB 1198 TACTTCACAGTGTGTCACGCGGCATTCATTCGATGCGGATTCCTGCTATTCACATAT 1257
QY 1503 GGAAGTGGGAAGATATGATGCTGACTGCTGCTGACCAATATTTGG 1547
DB 1258 GGAAGTGGGAAGTATTTAGATTTCTCTCTCCAAATGCTGATAGG 1302
RESULT 13
AAT69736/c
ID AAT69736 standard; DNA; 2165 BP.
XX
XX AAT69736;
XX
XX 10-SEP-1997 (first entry)
XX
XX Corn starch branching enzyme IIb gene fragment in pBB45.
XX
XX Starch branching enzyme IIb; SBEIIb; corn; maize; antisense; amylopectin;
XX transgenic plant; pBB45; ss.
XX
XX Zea mays.
OS
XX
XX MO9722703-A2.
XX
XX 26-JUN-1997.
XX

```
PF 12-DEC-1996; 96MO-US019678.
XX
XX 20-DEC-1995; 95US-0009113P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Hubbard NL, Klein TM, Broglie KE;
XX
XX WPI, 1997-341694/31.
XX
XX Transgenic corn in which grain derived starch fine structure is
XX PT controlled - specifically branch chain distribution of amylopectin,
XX PT useful in preparation of thickened foodstuff.
XX
XX Example 3; Page 55-56; 92pp; English.
XX
XX A.2.16 kb cDNA insert (AAT69736) in plasmid pBE45 comprises the entire 5'
XX untranslated region as well as 2.08 kb of the coding region of corn
XX starch branching enzyme IIb (SBEIIb) cDNA (see also AAT69729). It was
XX generated by EcoRI digestion of plasmid pBE240 and was inserted into
XX vector pM103 in antisense orientation with respect to a maize 27 kDa
XX zein promoter and a 10 kDa zein gene 3' sequence. Transgenic corn plants
XX expressing the near full-length SBEIIb antisense transcript demonstrated
XX a unique starch branching phenotype
XX
XX Sequence 2165 BP; 593 A; 580 C; 416 G; 576 T; 0 U; 0 Other;
XX
XX Query Match 5.4%; Score 110.6; DB 2; Length 2165;
XX Best Local Similarity 79.4%; Pred. No. 1.3e-15;
XX Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
XX
XX 1383 AGTATTGCTCAATATATACCTTGACGGTTTGATGGATGGACATACAT 1442
XX |||||
XX 950 AGTCATGCGTCAAGTATATATCTGTGATGGTGGATGGTACATACAT 891
XX |||||
XX 1443 TACTTCCACGGTGTGCACGCGGCATCATTTGATGGATTCGTCTATTCACTAT 1502
XX |||||
XX 890 TACTTTCAAGTGTGCACGTCGCATCATCTGATGGATTCGCTATTACTAT 831
XX |||||
XX 1503 GGGAGTTGGGAAGTATGAGCTCTGACTTGTGCACCATATTGG 1547
XX |||||
XX 830 GGGAACTGGGAAGTTTAAAGATTCTCTCCATGCTAGATGG 786
XX
XX RESULT 14
XX AAV70961
XX ID AAV70961 standard; DNA; 2640 BP.
XX
XX AC AAV70961;
XX
XX DT 23-AUG-1999 (first entry)
XX
XX DE DNA encoding maize branching enzyme II.
XX
XX KM Non-glycogen-like polysaccharide production; fermentation;
XX starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;
XX non-starch branching gene; amylopectin; amylose; plant-like starch;
XX maize branching enzyme II; ss.
XX
XX Zea mays.
XX
XX OS WO9844780-A1.
XX
XX PN 15-OCT-1998.
XX
XX PD 03-APR-1998; 98MO-US006660.
XX
XX PF 04-APR-1997; 97US-0042939P.
XX
XX PR (EXSE-) EXSEED GENETICS LLC.
XX
XX PA Hubbard NL, Klein TM, Broglie KE;
XX
XX PI Guan H, Keeling PL;
XX
XX
```

```
DR WPI, 1998-568285/48.
XX
XX P-PSDB; AAV70895.
XX
XX PT Producing non-glycogen-like polysaccharides in bacteria, fungi or plants
XX PT - transformed with genes for enzymes involved in starch or glycogen
XX PT synthesis allows fermentative production of starches with engineered
XX PT properties.
XX
XX PS Disclosure; Fig 53; 150pp; English.
XX
XX CC The specification describes a method for the production of non-glycogen-
XX CC like polysaccharides in a host. The method comprises transforming a host,
XX CC suitable for fermentation, with genes encoding starch- or glycogen-
XX CC synthesis enzymes, and fermenting the transformants. The specification
XX CC also describes hosts transformed with a gene active in glycogen synthesis
XX CC and at least one non-starch branching gene, involved in production of
XX CC amylopectin or amylose in its original host. The method is used to
XX CC produce plant-like starches by fermentation and new starches in plants.
XX CC These starches are useful for all food and non-food applications of
XX CC starch. The present sequence is used in the course of the invention
XX
XX SQ Sequence 2640 BP; 715 A; 510 C; 686 G; 729 T; 0 U; 0 Other;
XX
XX Query Match 5.4%; Score 110.6; DB 2; Length 2640;
XX Best Local Similarity 79.4%; Pred. No. 1.4e-15;
XX Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
XX
XX 1383 AGTCATTGCTCAATATATACCTTGACGGTTTGATGGATGGACATACAT 1442
XX |||||
XX 1143 AGTCATGCGTCAAGTATATATCTGTGATGGTGGATGGTACATACAT 1202
XX |||||
XX 1443 TACTTCCACGGTGTGCACGCGGCATCATTTGATGGATTCGTCTATTCACTAT 1502
XX |||||
XX 1203 TACTTTCAAGTGTGCACGTCGCATCATCTGATGGATTCGCTATTACTAT 1262
XX |||||
XX 1503 GGGAGTTGGGAAGTATGAGCTCTGACTTGTGCACCATATTGG 1547
XX |||||
XX 1263 GGGAACTGGGAAGTTTAAAGATTCTCTCCATGCTAGATGG 1307
XX
XX RESULT 15
XX AAT69729
XX ID AAT69729 standard; DNA; 2665 BP.
XX
XX AC AAT69729;
XX
XX DT 10-SEP-1997 (first entry)
XX
XX DE Plasmid pBE240 insert encoding corn starch branching enzyme IIb.
XX
XX KM Starch branching enzyme IIb; SBEIIb; corn; maize; antisense; amylopectin;
XX transgenic plant; pBE240; ss.
XX
XX Zea mays.
XX
XX OS Key Location/Qualifiers
XX FT 79,2478
XX FT CDS /*tag= a
XX
XX PN WO9722703-A2.
XX
XX PD 26-JUN-1997.
XX
XX PF 12-DEC-1996; 96MO-US019678.
XX
XX PR 20-DEC-1995; 95US-0009113P.
XX
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX PI Hubbard NL, Klein TM, Broglie KE;
XX
XX WPI, 1997-341694/31.
XX
XX P-PSDB; AAV19212.
XX
XX
```

XX Transgenic corn in which grain derived starch fine structure is
 PT controlled - specifically branch chain distribution of amylopectin,
 PT useful in preparation of thickened foodstuff.

PS Example 1; Page 50-53; 92pp; English.

CC A cDNA insert (AA169729) in plasmid clone pBE240 comprises a 2.7 kb EcoRI
 CC -XhoI fragment isolated from a corn cDNA library. It includes an open
 CC reading frame encoding starch branching enzyme 1b (SBE1b) (AA169729).
 CC The insert was used as a starting point in the assembly of DNA constructs
 CC (see also AA169730, AA169736-37) designed to achieve suppression of
 CC SBE1b expression in transgenic corn plants, and thereby to produce novel
 CC starches that have properties beneficial in food and industrial
 CC applications

XX Sequence 2665 BP; 700 A; 525 C; 705 G; 735 T; 0 U; 0 Other;

Query Match 5.4%; Score 110.6; DB 2; Length 2665;
 Best Local Similarity 79.4%; Pred. No. 1.4e-15;
 Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY	1383	AGTCATTCGTCAAATAATACCCCTTGACGGTTTGATGGTTGATGGCCTGATACACAT	1442
DB	1216	AGTCATGCGTCAGTATATCTGATGGTGAATGGTTGATGGTACAGATACACAT	1275
QY	1443	TACTTCACGGTGTCCACGGGCGCATTCATGGATGGGATTCCTGCTATTCACACTAT	1502
DB	1276	TACTTCACAGTGTCCACGGGCGCATTCATGGATGGGATTCCTGCTATTCACACTAT	1335
QY	1503	GGGAGTTGGAGATATAGCTCTGACTCTGTCCACATATTTGG	1547
DB	1336	GGGACTGGGAGATTTAAGATTCTCTCTCCAAATGCTAGATGG	1380

Search completed: April 10, 2004, 04:00:06
 Job time : 808.094 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 03:15:35 ; Search time 145.768 Seconds
(without alignments)
7804.525 Million cell updates/sec

Title: US-09-508-377-10_COPY_4818_6867

Perfect score: 2050

Sequence: 1 ccgaagaattcatatgc.....catgtgtaagatgtaagtg 2050

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	144.2	7.0	2853	4	US-09-609-040-3 Sequence 3, Appl1
2	122.2	6.0	2446	4	US-09-731-166-9 Sequence 9, Appl1
3	110.6	5.4	2087	4	US-09-257-894-9 Sequence 20, Appl1
4	110.6	5.4	2165	4	US-09-257-894-8 Sequence 8, Appl1
5	110.6	5.4	2665	4	US-09-257-894-11 Sequence 11, Appl1
6	110.6	5.4	2720	4	US-09-731-166-11 Sequence 11, Appl1
7	110.6	5.4	2725	3	US-08-941-445A-14 Sequence 14, Appl1
8	94	4.6	1393	3	US-09-087-277-3 Sequence 3, Appl1
9	94	4.6	1393	3	US-09-658-499-3 Sequence 3, Appl1
10	94	4.6	3074	4	US-09-087-277-1 Sequence 1, Appl1
11	94	4.6	3074	4	US-09-658-499-1 Sequence 1, Appl1
12	93.6	4.6	303	4	US-09-313-294A-6200 Sequence 6200, Ap
13	74.4	3.6	10322	3	US-09-330-330-3 Sequence 3, Appl1
14	71.2	3.5	1809	4	US-09-257-894-25 Sequence 25, Appl1
15	71.2	3.5	1865	4	US-09-257-894-20 Sequence 20, Appl1
16	71.2	3.5	2470	4	US-09-731-166-13 Sequence 13, Appl1
17	71.2	3.5	2487	4	US-09-257-894-19 Sequence 19, Appl1
18	71.2	3.5	2565	4	US-09-257-894-24 Sequence 24, Appl1
19	71.2	3.5	2763	4	US-08-941-445A-16 Sequence 16, Appl1
20	71.2	3.5	2772	4	US-09-257-894-12 Sequence 12, Appl1
21	67.8	3.3	2909	4	US-08-104-158-1 Sequence 1, Appl1
22	67.8	3.3	2909	4	US-09-609-040-1 Sequence 1, Appl1
23	67.8	3.3	3128	4	US-08-716-449-1 Sequence 1, Appl1
24	67.8	3.3	11469	4	US-09-367-895-29 Sequence 29, Appl1
25	67.8	3.3	11478	3	US-08-981-803-29 Sequence 29, Appl1

28	56.6	2.8	5402	4	US-09-221-017B-194 Sequence 194, App
29	54	2.6	807	1	US-08-165-315D-1 Sequence 1, Appl1
30	54	2.6	807	3	US-08-702-609A-2 Sequence 2, Appl1
31	54	2.6	846	1	US-08-165-315D-2 Sequence 2, Appl1
32	54	2.6	1327	1	US-08-165-315D-3 Sequence 3, Appl1
33	51.4	2.5	7218	1	US-08-232-463-14 Sequence 14, Appl1
34	49.6	2.4	1026	3	US-09-105-350-13 Sequence 13, Appl1
35	49.6	2.4	2169	3	US-09-105-350-5 Sequence 5, Appl1
36	48.8	2.4	6733	4	US-09-124-541-2 Sequence 2, Appl1
37	48.8	2.4	6733	4	US-09-663-336-2 Sequence 2, Appl1
38	47	2.3	658	3	US-08-998-416-555 Sequence 595, App
39	44.4	2.2	640681	4	US-09-790-968-1 Sequence 1, Appl1
40	44.2	2.2	4818	3	US-08-817-926-27 Sequence 27, Appl1
41	43.8	2.1	832	4	US-09-621-976-2813 Sequence 2813, Ap
42	43.8	2.1	832	4	US-09-621-976-2813 Sequence 2813, Ap
43	42.2	2.1	1026	3	US-09-105-350-13 Sequence 13, Appl1
44	42.2	2.1	2169	3	US-09-105-350-5 Sequence 5, Appl1
45	41.8	2.0	9347	4	US-10-204-708-35 Sequence 35, Appl1

ALIGNMENTS

RESULT 1									
US-09-609-040-3									
Sequence 3, Application US/09609040									
Patent No. 6570066									
GENERAL INFORMATION:									
APPLICANT: Wilmutzer, et al.									
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRAT									
FILE REFERENCE: 514413-3515.1									
CURRENT APPLICATION NUMBER: US/09/609,040									
PRIOR APPLICATION NUMBER: 2000-06-30									
PRIOR FILING DATE: 1992-02-11									
NUMBER OF SEQ ID NOS: 4									
SOFTWARE: PatentIn version 3.0									
SEQ ID NO 3									
LENGTH: 2853									
TYPE: DNA									
ORGANISM: Triticum aestivum									
FEATURE:									
NAME/KEY: CDS									
LOCATION: (313)..(2499)									
OTHER INFORMATION: BRANCHING ENZYME									
US-09-609-040-3									
Query Match									
Best local Similarity 72.8%; Pred. No. 1.9e-28;									
Matches 244; Conservative 0; Mismatches 3; Indels 88; Gaps 1;									
QY	1383	AGTCATTCGTC	AAATTAATACCCTTGACCGTTG	AAATGTTTGATGTTGATGACGACATACACAT	1442				
DB	1240	AGTCATTCGTC	CAATAATACCCTTGACCGTTG	AAATGTTTGATGTTGATGACGACATACACAT	1299				
QY	1443	TACTTCACG	TGTTCCACGGCGGCATCATGATG	GGATTCGTTCTATTCACATAT	1502				
DB	1300	TACTTCACG	TGTTCCACGGCGGCATCATGATG	GGATTCGTTCTATTCACATAT	1359				
QY	1503	GGGAGTGG	AGATAGTAACTCTGACTTCGT	GCACCATATTTGGCTAACTGCTGTT	1562				
DB	1360	GGGAGTGG	AGATAGTAACTCTGACTTCGT	GCACCATATTTGGCTAACTGCTGTT	1371				
QY	1563	AAATCTGTT	TACACATGTTGATATTTCTATTC	AGATGATGATTTCTTACTGTC	1622				
DB	1372	-----	-----	-----	1391				
QY	1623	AAACGAGAT	GGTGGCTTGAAGATATAAGTTG	ATGATGATTTGATGGGATGAC	1682				
DB	1392	AAACGAGAT	GGTGGCTTGAAGATATAAGTTG	ATGATGATTTGATGGGATGAC	1451				

DB 1452 CTCGATGATGTATCTCACCATTGATTAACAATCA 1486

RESULT 2

US-09-731-166-9
Sequence 9, Application US/09731166
Patent No. 6639126
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccharides
FILE REFERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
PRIOR FILING DATE: 2000-12-06
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 2446
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: SBE11a
NAME/KEY: CDS
LOCATION: (2)...(2446)
US-09-731-166-9

Query Match 6.0%; Score 122.2; DB 4; Length 2446;
Best Local Similarity 88.1%; Pred. No. 1.2e-22;
Matches 133; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

DB 1383 AGTCATTCGTCGAATATATACCCCTTGACGGTGGTTCGATGGACATGATACAT 1442
1172 AGTCATTCGAATATATATACCTTGATGGATGGTTCGATGGACATGATACAT 1231
QY 1443 TACTTCCAGGTGGTCCACGGCCCATTCATGATGGATTCCTCTATTCATCAT 1502
DB 1232 TACTTCCATGGTGTCCACGGCCCATTCATGATGGATTCCTCTATTCATCAT 1291
QY 1503 GGGAGTTGGGAAGTATGATGCTTGACTTCT 1533
DB 1292 GGGAGTTGGGAAGTATGATGCTTGACTTCT 1322

RESULT 3

US-09-257-894-9
Sequence 9, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: NO. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95

SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-257-894-9

Query Match 5.4%; Score 110.6; DB 4; Length 2087;
Best Local Similarity 79.4%; Pred. No. 1.4e-19;
Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

DB 1383 AGTCATTCGTCGAATATATACCCCTTGACGGTGGTTCGATGGACATGATACAT 1442
1138 AGTCATTCGAATATATATACCTTGATGGATGGTTCGATGGACATGATACAT 1197
QY 1443 TACTTCCAGGTGGTCCACGGCCCATTCATGATGGATTCCTCTATTCATCAT 1502
DB 1198 TACTTCCAGGTGGTCCACGGCCCATTCATGATGGATTCCTCTATTCATCAT 1257
QY 1503 GGGAGTTGGGAAGTATGATGCTTGACTTCTGACCATATTTGG 1547
DB 1258 GGGAGTTGGGAAGTATGATGCTTGACTTCTGACCATATTTG 1302

RESULT 4

US-09-257-894-8/c
Sequence 8, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: NO. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998

Mon Apr 12 10:24:24 2004

us-09-508-377-10_copy_4818_6867.rml

Page 3

ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-257-894-8

Query Match 5.4%; Score 110.6; DB 4; Length 2165;
Best Local Similarity 79.4%; Pred. No. 1.4e-19;
Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1383 AGTCATTGCTCAATATATACCTTGACGGTTTGATGTTTCGATGCGACATGATACAT 1442
DB 950 AGTCATGCGCTCAAGTAATATCTGATGGTGGTGGATGTTGATGTCATGATACAT 891
QY 1443 TACTTCACAGGTGGTCCACGCGGCATCATTGATGGGATTCGTCATTTCACTAT 1502
DB 890 TACTTCACAGGTGGTCCACGCGGCATCATTGATGGGATTCGTCATTTCACTAT 831
QY 1503 GGGAGTTGGGAAGTATGATGCTGCTGACTTCTGTCCACATATTTGG 1547
DB 830 GGGAGTTGGGAAGTATGATGCTGCTGACTTCTGTCCACATATTTGG 786

RESULT 5
US-09-257-894-1
Sequence 11, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore W.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
NUMBER OF INVENTION: 25
TITLE OF INVENTION: Expression of Starch Biosynthesis
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164

SEQUENCE CHARACTERISTICS:
LENGTH: 2665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 79..2476
US-09-257-894-1

Query Match 5.4%; Score 110.6; DB 4; Length 2665;
Best Local Similarity 79.4%; Pred. No. 1.6e-19;
Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1383 AGTCATTGCTCAATATATACCTTGACGGTTTGATGTTTCGATGCGACATGATACAT 1442
DB 1216 AGTCATGCGCTCAAGTAATATCTGATGGTGGTGGATGTTGATGTCATGATACAT 1275
QY 1443 TACTTCACAGGTGGTCCACGCGGCATCATTGATGGGATTCGTCATTTCACTAT 1502
DB 1276 TACTTCACAGGTGGTCCACGCGGCATCATTGATGGGATTCGTCATTTCACTAT 1335
QY 1503 GGGAGTTGGGAAGTATGATGCTGCTGACTTCTGTCCACATATTTGG 1547
DB 1336 GGGAGTTGGGAAGTATGATGCTGCTGACTTCTGTCCACATATTTGG 1380

RESULT 6
US-09-731-166-11
Sequence 11, Application US/09731166
Patent No. 6639126
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccharides
FILE REFERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2720
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc. feature
LOCATION: (0)..(0)
OTHER INFORMATION: SBRlib
OTHER INFORMATION: Genbank Accession No. 6639126 AF072725
NAME/KEY: CDS
LOCATION: (101)..(2500)
US-09-731-166-11

Query Match 5.4%; Score 110.6; DB 4; Length 2720;
Best Local Similarity 79.4%; Pred. No. 1.6e-19;
Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1383 AGTCATTGCTCAATATATACCTTGACGGTTTGATGTTTCGATGCGACATGATACAT 1442
DB 1238 AGTCATGCGCTCAAGTAATATCTGATGGTGGTGGATGTTGATGTCATGATACAT 1297
QY 1443 TACTTCACAGGTGGTCCACGCGGCATCATTGATGGGATTCGTCATTTCACTAT 1502
DB 1298 TACTTCACAGGTGGTCCACGCGGCATCATTGATGGGATTCGTCATTTCACTAT 1357
QY 1503 GGGAGTTGGGAAGTATGATGCTGCTGACTTCTGTCCACATATTTGG 1547
DB 1358 GGGAGTTGGGAAGTATGATGCTGCTGACTTCTGTCCACATATTTGG 1402

RESULT 7
US-08-941-445A-14
; Sequence 14, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Haining
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2725 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: mRNA
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 91..264
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 265..2487
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..2490
; US-08-941-445A-14

Query Match
Best Local Similarity 5.4%; Score 110.6; DB 3; Length 2725;
Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

DB 1383 AGTCATTGCTCAATATATACCTTGAAGGTTTGAATGGTTGCGACCTGATACACAT 1442
DB 1228 AGTCAGCGGCAAGTATATCTCGAGGAGGTTGATGTTGATGATACAGATACACAT 1287
DB 1443 TACTTCACAGGTGTCACGCGGCATCATGTGATGAGGATTCCTGCTATTAACATAT 1502
DB 1288 TACTTTCACAGTGTGTCACGCGGCATCATGTGATGAGGATTCCTGCTATTAACATAT 1347
DB 1503 GGGAGTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1547
DB 1348 GGGAACTGGGAGATTATTAATTTCTTCTCTCAATGCTAGATGG 1392

RESULT 8
US-09-087-277-3
; Sequence 3, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNODI, Jamsheed
; APPLICANT: LARSSON, Claas-Tomas
; APPLICANT: LARSSON, Hakar
; APPLICANT: PASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087,277B
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: beil gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (890)..(892)
; OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
; US-09-087-277-3

Query Match
Best Local Similarity 4.6%; Score 94; DB 3; Length 1393;
Matches 112; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

DB 1909 TTCTAGATGACATTACTTACTGCGGAACTATGCGGAATATTTGATTTGCTACTGATGTTGAT 1968
DB 734 TTATGGGTGGGATTCATCTGGGAACTACGAGATATCTTTGACTCGCACTGATGTGAT 793
DB 1969 GCGGTAGTTTACTGATGCTGTGTCACGATCTTAATTCATGAGACTTATCTGATGCTGTA 2028
DB 794 GCTGTGTGATCTGATGCTGTGTCACGATCTTATTCATGAGGCTTTCCAGATGCAAT 853
DB 2029 TCCATTGCTGAAGATGATGATG 2050
DB 854 ACCATTGATGAAGATGTTAGCG 875

RESULT 9
US-09-658-499-3
; Sequence 3, Application US/09658499

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/ Patent No. 6469231
/ GENERAL INFORMATION:
/ APPLICANT: EK, Bo
/ APPLICANT: KHOSNODI, Jamshid
/ APPLICANT: LARSSON, Clas-Tomas
/ APPLICANT: LARSSON, Hakan
/ APPLICANT: RASK, Lars
/ TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
/ FILE REFERENCE: 003300-486
/ CURRENT APPLICATION NUMBER: US/09/658,499
/ PRIOR FILING DATE: 1996-04-19
/ PRIOR APPLICATION NUMBER: SE 9601506-0
/ PRIOR FILING DATE: 1995-11-29
/ PRIOR APPLICATION NUMBER: PCT/SE96/01558
/ PRIOR FILING DATE: 1996-05-29
/ PRIOR FILING DATE: 1996-11-28
/ PRIOR APPLICATION NUMBER: SE 9504272-7
/ PRIOR FILING DATE: 1995-11-29
/ PRIOR APPLICATION NUMBER: SE 9601506-0
/ PRIOR FILING DATE: 1996-04-19
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 1393
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism:beli gene fragment
/ OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
/ OTHER INFORMATION: (potato)
/ NAME/KEY: CDS
/ LOCATION: (2)..(1393)
/ NAME/KEY: misc.feature
/ LOCATION: (424)..(1150)
/ OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
/ OTHER INFORMATION: C, G or T.
/ NAME/KEY: misc.feature
/ LOCATION: (422)..(424)
/ OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
/ NAME/KEY: misc.feature
/ LOCATION: (890)..(892)
/ OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
/ OTHER INFORMATION: or Phe.
/ NAME/KEY: misc.feature
/ LOCATION: (1148)..(1150)
/ OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
/ US-09-658-499-3
/
/ Query Match 4.6%; Score 94; DB 4; Length 1393;
/ Best Local Similarity 78.9%; Pred. No. 2,9e-15;
/ Matches 112; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
/
/ QY 1909 TTCTAGATGACATTCTGCGAAGTATGCGGATATTTGGATTGCTAGTGTGAT 1968
/ DB 734 TTATCGGTGGATTCCTGCGAAGTATGCGGATATTTGGATTGCTAGTGTGAT 793
/
/ QY 1969 GCGGTAGTTACTTGTGATGCTGTCACGATCTAATTCATGAGCTTATCCGATGCTGTA 2028
/ DB 794 GCTGTGTATCTGATGCTGTCACGATCTAATTCATGAGCTTATCCGATGCAATT 853
/
/ QY 2029 TCCATTGGTGAAGATGTAAGTG 2050
/ DB 854 ACCATTGGTGAAGATGTAAGTG 875
/
/ RESULT 10
/ US-09-087-277-1
/ Sequence 1, Application US/09087277B
/ Patent No. 6169226
/ GENERAL INFORMATION:
/ APPLICANT: EK, Bo
/ APPLICANT: KHOSNODI, Jamshid
/ APPLICANT: LARSSON, Clas-Tomas
/ APPLICANT: LARSSON, Hakan
```

```
/ APPLICANT: RASK, Lars
/ TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
/ FILE REFERENCE: 003300-486
/ CURRENT APPLICATION NUMBER: US/09/087,277B
/ PRIOR FILING DATE: 1996-05-29
/ PRIOR APPLICATION NUMBER: PCT/SE96/01558
/ PRIOR FILING DATE: 1996-11-28
/ PRIOR APPLICATION NUMBER: SE 9504272-7
/ PRIOR FILING DATE: 1995-11-29
/ PRIOR APPLICATION NUMBER: SE 9601506-0
/ PRIOR FILING DATE: 1996-04-19
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 3074
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism:beli gene
/ OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
/ OTHER INFORMATION: (potato)
/ NAME/KEY: CDS
/ LOCATION: (189)..(2825)
/ NAME/KEY: sig_peptide
/ LOCATION: (189)..(332)
/ NAME/KEY: mat_peptide
/ LOCATION: (333)..(2825)
/ NAME/KEY: misc.feature
/ LOCATION: (92)..(2156)
/ OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
/ OTHER INFORMATION: n wherein n = A, C, G or T.
/ NAME/KEY: misc.feature
/ LOCATION: (285)..(287)
/ OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
/ OTHER INFORMATION: or Phe.
/ NAME/KEY: misc.feature
/ LOCATION: (1407)..(1406)
/ OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
/ NAME/KEY: misc.feature
/ LOCATION: (1428)..(1430)
/ OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
/ NAME/KEY: misc.feature
/ LOCATION: (1896)..(1898)
/ OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
/ OTHER INFORMATION: or Phe.
/ NAME/KEY: misc.feature
/ LOCATION: (2154)..(2156)
/ OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
/ US-09-087-277-1
/
/ Query Match 4.6%; Score 94; DB 3; Length 3074;
/ Best Local Similarity 78.9%; Pred. No. 4,2e-15;
/ Matches 112; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
/
/ QY 1909 TTCTAGATGACATTCTGCGAAGTATGCGGATATTTGGATTGCTAGTGTGAT 1968
/ DB 1740 TTATCGGTGGATTCCTGCGAAGTATGCGGATATTTGGATTGCTAGTGTGAT 1799
/
/ QY 1969 GCGGTAGTTACTTGTGATGCTGTCACGATCTAATTCATGAGCTTATCCGATGCTGTA 2028
/ DB 1800 GCTGTGTATCTGATGCTGTCACGATCTAATTCATGAGCTTATCCGATGCAATT 1859
/
/ QY 2029 TCCATTGGTGAAGATGTAAGTG 2050
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,330
FILING DATE: 11-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 10-181455
FILING DATE: 12-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06501/032001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10322 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-330-330-3

Query Match 3.6%; Score 74.4; DB 3; Length 10322;
Best Local Similarity 63.6%; Pred. No. 1.2e-09;
Matches 145; Conservative 0; Mismatches 81; Indels 2; Gaps 2;

QY 961 TTGTGCTTAAGTCAAACTTTTAAGTTGACCAAGCTCTATTGAAATATATACATC 1020
DB 4998 TTTTTCAGTCAAACTTCCTT-AGTTGACCAAGTTATACAAAATTTTACACATA 5056
QY 1021 TACAACACCAATTACTTTGATCAGAT-TACAAATTTTATTTATATATAGCAATC 1079
DB 5057 TCCACACGAAATTAAGTTTCAATTAATGATGCAATTAATATTTGATGATGTTGT 5116
QY 1080 TTGTATGTTGATGATATGACACATTTTCTATAGACTTGTCAAATATAGAGAAGTTG 1139
DB 5117 TTTGTTGAATGATGCTGCTATATTTTAAAAAACTTGTCAAACCTAAACAAGTTG 5176
QY 1140 ACTTGACAAATCTAGAACTTCAATCAATTTGGATGACAGGGAACAT 1187
DB 5177 ACTAGAGAAAAGTCGAAACGACTTATATATGAAATAGAGGGAAGAT 5224

RESULT 14

US-09-257-894-25
Sequence 25, Application US/09257894
Patent No. 6376749

GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
NAME: Majarian, William R.

APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-257-894-25

Query Match 3.5%; Score 71.2; DB 4; Length 1809;
Best Local Similarity 69.3%; Pred. No. 3.7e-09;
Matches 97; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 271 TTGTGTTGGCTTTCACAGTACCATGTTACTAATTTTTCACCAAGTGCCTTT 330
DB 895 TCGTACTATGCTTCTTTCGGGTACCATGTCACAAATTTCTTGGCGTTAGCGACATCA 954
QY 331 GGAATCCAGAGACTTAAATCCTTGATGATGATGAGACATGAGCTGGTGTGTT 390
DB 955 GGCACACAGAGAGCTTCAATATCTTGTATTAAGGACACAGTTGGGTTTGCAGTT 1014
QY 391 CTATGATATTTGTTCAATAG 410
DB 1015 CTGATGATGTTGTCATAG 1034

RESULT 15

US-09-257-894-20
Sequence 20, Application US/09257894
Patent No. 6376749

GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.

Mon Apr 12 10:24:24 2004

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Page 8

/ REGISTRATION NUMBER: 41,173
/ REFERENCE/DOCKET NUMBER: BB-1066-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4926
/ TELEFAX: 302-773-0164
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1865 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-09-257-894-20

Query Match 3.5%; Score 71.2; DB 4; Length 1865;
Best Local Similarity 69.3%; Pred. No. 3.8e-09;
Matches 97; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
QY 271 TTGTTGTTGCGCTTGTTCAGGTACCATGTTACTAATTTTTCACCAAGTAGCCGTTT 330
Db 951 TCGTACTATGCTTCTTTCGGGTACCATGTGACAAATTTCTTCCGGTTAGCAGCATCA 1010
QY 331 GGAAGTCCAGAGAGACTTAAATCCTTGATCGATAGAGCAGCATGAGCTTGGTTGTTGTT 390
Db 1011 GGCACACAGAGAGAGCTCAATATCTGTGTATAGGACACAGTTGGGTTTGGAGTT 1070
QY 391 CTTATGATATGTTCTCATAG 410
Db 1071 CTGATGATGTTGTCCATAG 1090

Search completed: April 10, 2004, 14:13:12
Job time : 150.768 secs

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Db	6024	ATCATATATTTGATGTTCCCTGTGATCCAAATATGATTAAGTTCTAGATTTCCTCTAA	5965
Qy	971	GTCAAATCTTTTAACTTACCAAGCCTCTGGAAATATATCAATATCAACAACCA	10930
Db	5964	GTCAAATCTTCTATATTTGACCAAGCTATAGAAAATGCTGATATCTACAACATCA	59050
Qy	1031	AATTACTTGTATGATTAACAATTTTATTATTATTAATTATGACATCTTTGATGTGT	10900
Db	5904	AAGATGTCATATATATATATATATATATTTGTTATGTGATCAAGAATATTTGGTGTTGT	58458

Db 5844 AGATGTTGATATATTTTCCAAATAGACTTGGTCAAACTTAAAGAGTTTGACCTTAGGACAA 57855

Db 5784 ATGAAGAAGCTTAACTAATATGTTCAATGAATTCACAGGGAAGTACAT 5734

RESULT 4
US-10-260-238-1027
; Sequence 1027, Application US/10260238

?
 ? PUBLICATION NO: C86097000000000000000
 ? GENERAL INFORMATION:
 ? APPLICANT: Budworth, Paul R.
 ? APPLICANT: Moughamer, Todd G.

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APPLICANT: Katagiri, Fumiyaki
 APPLICANT: Kreps, Joel
 APPLICANT: Provart, Nicholas
 APPLICANT: Ricke, Darrell

APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238

PRIOR APPLICATION NUMBER: US 60/325,448
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: US 60/325,277

1 PRIOR APPLICATION NUMBER: US 60/370,620
 2
 3 PRIOR FILING DATE: 2002-04-04
 4
 5 NUMBER OF SEQ ID NOS: 6077
 6

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: SEQ ID NO 1027
: LENGTH: 1642
: TYPE: DNA
: ORGANISM: Oryza sativa

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Query Match	5.5%;	Score 112.4;	DB 15;	length 1642;
Best Local Similarity	83.1%;	Pred. No. 1.3e-15;		
US-10-260-238-1027				

Matches	128;	Conservative	0;	Mismatches	26;	Indels	0;	Gaps	0;
0y	1373	TGPAACCCGACAGCATTCGTCAATAATATACCCTGACGGTTGAATGATGTTTCGATGGCAC	1432						

Db	323	TGATCACAAGACCCATGCGTCAAAATAATATACCCATAGATGGGTGAAACGGTTTGTGCTAC	382
Qy	1433	TGATACCATTTCTTCCACGGTGGTCCACGGGGCCATCATTTGGATGTGGGATTTCTCGTAT	1492

Db 383 AAGATACCGATTACTTTCATAGTGGTTTCAACGGGCGCATCATTTGATGTGGATTTCGGCT 442

Qy 1493 ATTCAACTATGGGAGTGTGGAGATATGTAGCTCT 1526

Db 443 TTCACTATGGGATTTGGAGCTTCAGATT 475

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US-10-434-893A-4
; Sequence 4, Application US/10434893A
; Publication No. US20040060083A1

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RESULT 8
US-09-792-127-1

/ Sequence 1, Application US/09792127
/ Patent No. US2002002713A1
/ GENERAL INFORMATION:
/ APPLICANT: Allen, Steve
/ APPLICANT: Beckles, Diane M.
/ APPLICANT: Butler, Karla
/ APPLICANT: Pearlstein, Rich
/ TITLE OF INVENTION: Starch Branching Enzyme IIb
/ FILE REFERENCE: B01439 US NA
/ CURRENT APPLICATION NUMBER: US/09/792,127
/ PRIOR FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 60/186098
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO: 1
/ LENGTH: 2559
/ TYPE: DNA
/ ORGANISM: Triticum aestivum
US-09-792-127-1

Query Match 5.1%; Score 105; DB 9; Length 2559;
Best Local Similarity 82.8%; Pred. No. 8.8e-14;
Matches 120; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

DB 1382 CAGTCAATTCGTAATTAATACCTTACCGTTTGAATGGTTTCGATGCGACTGATACACA 1441
|||
QY 1442 TTACTTCCACGGTGTGTCACGCGGCCATCATTTGATGGATTTCTGCTTATTAACA 1501
|||
DB 887 TTACTTCCACGGTGTGTCACGCGGCCATCATTTGATGGATTTCTGCTTATTAACA 946
|||
QY 1502 TGGGAGTTGGGAAGTATGAGCTCT 1526
|||
DB 947 TGGGAATAGGAAGTATTAAGTTT 971
|||

RESULT 9
US-09-792-127-3

/ Sequence 3, Application US/09792127
/ Patent No. US2002002713A1
/ GENERAL INFORMATION:
/ APPLICANT: Allen, Steve
/ APPLICANT: Beckles, Diane M.
/ APPLICANT: Butler, Karla
/ APPLICANT: Pearlstein, Rich
/ TITLE OF INVENTION: Starch Branching Enzyme IIb
/ FILE REFERENCE: B01439 US NA
/ CURRENT APPLICATION NUMBER: US/09/792,127
/ PRIOR FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 60/186098
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO: 3
/ LENGTH: 3039
/ TYPE: DNA
/ ORGANISM: Triticum aestivum
US-09-792-127-3

Query Match 5.1%; Score 105; DB 9; Length 3039;
Best Local Similarity 82.8%; Pred. No. 9.7e-14;
Matches 120; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1382 CAGTCAATTCGTAATTAATACCTTACCGTTTGAATGGTTTCGATGCGACTGATACACA 1441
|||
DB 1307 CAGTCAACGGGTCAATTAATACCTTACCGTTTGAATGGTTTCGATGCGACTGATACACA 1366
|||

DB 1367 TTACTTCATGCGCGTTTACCGGCCATCATTTGATGGATTTCCCGTGTATTA 1426
|||
QY 1502 TGGGAGTTGGGAAGTATGAGCTCT 1526
|||
DB 1427 TGGGAATAGGAAGTATTAAGTTT 1451
|||

RESULT 10
US-10-434-893A-2

/ Sequence 2, Application US/10434893A
/ Publication No. US20040060083A1
/ GENERAL INFORMATION:
/ APPLICANT: Ahmed Regina
/ APPLICANT: Matthew Kennedy Morell
/ APPLICANT: Sadequr Rahman
/ TITLE OF INVENTION: Barley with altered starch branching enzyme activity and starch and sta
/ FILE REFERENCE: 69425
/ CURRENT APPLICATION NUMBER: US/10/434,893A
/ PRIOR FILING DATE: 2003-05-09
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn version 2.1
/ SEQ ID NO: 2
/ LENGTH: 2780
/ TYPE: DNA
/ ORGANISM: Hordeum vulgare
/ FEATURE:
/ OTHER INFORMATION: SSBEIIb CDNA
US-10-434-893A-2

Query Match 5.0%; Score 101.8; DB 12; Length 2780;
Best Local Similarity 77.0%; Pred. No. 5.1e-13;
Matches 124; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 290 GGTACCATGTTACTAATTTTTCGACCAAGTACCGTTTGAATCCGAGAGACTTAA 349
|||
DB 1115 GGTACCATGTTACTAATTTTTCGACCAAGTACCGTTTGAATCCGAGAGACTTAA 1174
|||
QY 350 AATCCTTGATGATGAGACACATGAGCTTGTCTGCTTGTATGATGATTTGATTA 409
|||
DB 1175 AATCCTTGATGATGAGACACATGAGCTTGTCTGCTTGTATGATGATTTGATTA 1234
|||
QY 410 GGTAAATAGTCCAAATTTTATTTTATGCTTTTATGCTTTAT 450
|||
DB 1235 GTCAAGCATCAAGTAAATACCTTGGACGGTTGAATGATTTT 1275
|||

RESULT 11
US-10-260-238-2253/C

/ Sequence 2253, Application US/10260238
/ Publication No. US20040016025A1
/ GENERAL INFORMATION:
/ APPLICANT: Budworth, Paul R.
/ APPLICANT: Moughamer, Todd G.
/ APPLICANT: Briggs, Steven P.
/ APPLICANT: Cooper, Bret
/ APPLICANT: Glazebrook, Jane
/ APPLICANT: Goff, Stephen A.
/ APPLICANT: Katagiri, Fumiyaki
/ APPLICANT: Krieds, Joel
/ APPLICANT: Provart, Nicholas
/ APPLICANT: Rieke, Darrell
/ APPLICANT: Zhu, Tong
/ TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
/ FILE REFERENCE: 60111-NP
/ CURRENT APPLICATION NUMBER: US/10/260,238
/ PRIOR FILING DATE: 2002-09-26
/ PRIOR APPLICATION NUMBER: US 60/325,448
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: US 60/325,277
/ PRIOR FILING DATE: 2001-09-26

QY 1382 CAGTCAATTCGTAATTAATACCTTACCGTTTGAATGGTTTCGATGCGACTGATACACA 1441
|||
DB 1307 CAGTCAACGGGTCAATTAATACCTTACCGTTTGAATGGTTTCGATGCGACTGATACACA 1366
|||

Mon Apr 12 10:24:24 2004

us-09-508-377-10_copy_4818_6867.rnpb

Page 7

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Matches 112; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1909 TTCTAGATGACATTTACTGGGAGACATGCGAATATTTTGGATTTGCTACTGATGTGAT 1968
Db 734 TTATCGGCGGATTCACCTGCGAAGACAGAGAACTTTGAGCTGCGAAGCTGATGTGAT 793
QY 1969 GCGGTAGTTACTTGATGCTGCTCAACGATCTAATTCATGAGCTTTATCTGATGCTGA 2028
Db 794 GCTGTGTGATCTGATCTGCTGCTCAACGATCTTATTCATGAGGCTTTCCAGATGCAAT 853
QY 2029 TCCATTGCTGAAGATGTAAGTG 2050
Db 854 ACCATTGCTGAAGATGTTAGCG 875

RESULT 14
US-10-260-238-2424
; Sequence 2424, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Karagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 2424
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-2424

Query Match 4.6%; Score 94; DB 15; Length 2000;
Best Local Similarity 62.0%; Pred. No. 2,8e-11;
Matches 165; Conservative 0; Mismatches 100; Indels 1; Gaps 1;
QY 940 CATATTTACTTAAAGTTCTTCATTTGCTCTAGTCAACATCTTTTAAAGTTTGACCAAGTCT 999
Db 512 CAGGTTATTAAGATGTTTAACTTTAGTTCAGAGTCAAACTTTTCAAGTTTGACTAAGTTT 571
QY 1000 ATTGAAAATATATCAACATCTACACACACCAATTTCTTGATCAGATTTTACAATTTTA 1059
Db 572 AGAGCATATATATATATATATATATATATATATATATATATATATATATATATATAT 630
QY 1060 TTTTATTTATTTAGCAGATCTTTGATGTTGTAGATATCAGACATTTTCTATAGACTTG 1119
Db 631 TATATTTTATATATATATTTGCTTGGGTTGAATGTTACTACTTTTCTTACAACTTG 690
QY 1120 GTCAATATAGAGAGTTGACTTAGACAAATCTAGAACTTCAATCAATTTGGATGAGA 1179
Db 691 ATCAAACTTAAAGCGTTTGGCTTTGATCAAAAGTCAAAAGCTTTAAACCTGAAAAGGA 750
QY 1180 GGAACATCAATTAATATAGATAGAT 1205
Db 751 GGGAGTACATTAATTTTGAATTAAT 776
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RESULT 15
US-10-056-454A-16
; Sequence 16, Application US/10056454A
; Publication No. US20030166919A1
; GENERAL INFORMATION:
; APPLICANT: National Starch and Chemical Investment Holding Corporation
; TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: National Starch and Chemical Investment Holding Corporation
; STREET: 1000 Unidema Blvd.
; CITY: Newcastle
; STATE: Delaware
; COUNTRY: United States of America
; ZIP: 19720
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/056,454A
; FILING DATE: 25-Jun-2002
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-056-454A-16

Query Match 4.6%; Score 94; DB 14; Length 2576;
Best Local Similarity 78.9%; Pred. No. 3.2e-11;
Matches 112; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1909 TTCTAGATGACATTTACTGGGAGACATGCGAATATTTTGGATTTGCTACTGATGTGAT 1968
Db 1471 TTATCGGCGGATTCACCTGCGAAGACAGAGAACTTTGAGCTGCGAAGCTGATGTGAT 1530
QY 1969 GCGGTAGTTACTTGATGCTGCTCAACGATCTAATTCATGAGCTTTATCTGATGCTGA 2028
Db 1531 GCTGTGTGATCTGATCTGCTGCTCAACGATCTTATTCATGAGGCTTTCCAGATGCAAT 1590
QY 2029 TCCATTGCTGAAGATGTAAGTG 2050
Db 1591 ACCATTGCTGAAGATGTTAGCG 1612
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Search completed: April 10, 2004, 20:07:35
Job time : 729.03 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 03:15:20 ; Search time 5409.32 seconds
(without alignments)
11317.033 Million cell updates/sec

Title: US-09-508-377-10_COPY_4818_6867

Perfect score: 2050

Sequence: 1 ccgaagataatcatcatgc.....catgtggaagatgtaagtg 2050

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estin:*
4: em_estma:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vtc:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rdd:*
26: em_gss_dhg:*
27: em_gss_vtl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	250.8	12.2	930	28	CC362748 PUHLB23TD
C 2	183.8	9.0	985	29	CG882826 ZMMBB049
3	140	6.8	527	6	AL812818 Triticum
4	139.4	6.8	476	13	BU972445 HB21K16r

5	139.4	6.8	537	13	BU967331	BU967331 HB03P08r
6	134	6.5	476	13	BO245037	BO245037 TAB15032A
7	134	6.5	623	13	BU986646	BU986646 HFI2102r
8	133.2	6.5	610	28	AO576669	AO576669 nbxb0089J
9	132.4	6.5	621	14	CD890409	CD890409 G118.114J
10	125.8	6.1	628	9	AV939010	AV939010 AV939010
11	124.4	6.1	411	13	BU970967	BU970967 HB16D15r
12	123.2	6.0	618	14	CA292638	CA292638 SCRLFL802
13	123.2	6.0	650	14	CA202517	CA202517 SCRRFL102
14	122.2	6.0	2766	11	AY109521	AY109521 Zee maye
15	121.6	5.9	399	12	BM660711	BM660711 952041B07
16	121.6	5.9	595	13	CA188662	CA188662 SCCCAM205
17	121.6	5.9	690	13	CA083722	CA083722 SCEPMAM20
18	120.4	5.9	520	28	B2348549	B2348549 hp58f11.9
19	120.4	5.9	578	28	B2348550	B2348550 hp58f11.9
20	119.4	5.8	649	13	BQ840703	BQ840703 WHB4202_E
21	118.8	5.8	550	13	BU966891	BU966891 HB02K24r
22	113.8	5.6	541	29	AG213031	AG213031 Oryza sat
23	113.2	5.5	462	10	BF585594	BF585594 FM1_23.CO
24	113.2	5.5	479	28	AO856076	AO856076 nbxb0064F
25	113.2	5.5	821	28	AO840558	AO840558 nbxb0064F
26	112.6	5.5	682	14	CD938053	CD938053 OV_108019
27	110.6	5.4	852	14	CD438018	CD438018 ELO1N0508
28	110.6	5.4	871	14	CD444875	CD444875 ELO1N0445
29	110.6	5.4	2732	11	AY109532	AY109532 Zee maye
30	110.4	5.4	781	28	AO574595	AO574595 nbxb0085D
31	110.4	5.4	882	14	CB632953	CB632953 OST1Pb11
32	110	5.4	420	9	AJ465766	AJ465766 AJ465766
33	110	5.4	872	28	BZ667957	BZ667957 PUBM33TD
34	108.8	5.3	440	28	BZ667903	BZ667903 PUBM33TD
35	108.8	5.3	578	28	B2348550	B2348550 hp58f11.9
36	108.2	5.3	520	28	B2348549	B2348549 hp58f11.9
37	108.2	5.3	678	14	CA191146	CA191146 SCCCR7C0
38	108.2	5.3	821	28	AO840558	AO840558 nbxb0064F
39	107.4	5.2	697	29	CC992767	CC992767 ZUEN43TV
40	107.4	5.2	736	14	CD444184	CD444184 ELO1N0436
41	106.4	5.2	548	14	CD888421	CD888421 G118.1070
42	105.6	5.2	424	14	T23385	T23385 Sc09b11.mem
43	105.4	5.1	402	12	BM660712	BM660712 952041B07
44	105.2	5.1	576	10	AW244197	AW244197 687050P06
45	105.2	5.1	636	14	CA255656	CA255656 SCEPFL418

ALIGNMENTS

RESULT 1
CC362748/c
LOCUS
DEFINITION
930 bp DNA linear GSS 16-MAY-2003
PUHLB23TD_ZM_0_6_1_0_KB_Zee maye genomic clone ZMMBT8475D22,
genomic survey sequence.
ACCESSION
CC362748
VERSION
CC362748.1 GI:30832148
KEYWORDS
GSS.
SOURCE
Zee maye
ORGANISM
Zea mays
Bokaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 930)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
JOURNAL
Other GSSs: PUHLB23TB
COMMENT
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP

Class: sheared ends.
 Location/Qualifiers
 source
 1. 930
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMB0492B17"
 /clone_1db="ZM 0.6-1.0 KB"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
 Cor selected genomic DNA library"

ORIGIN
 Query Match 12.2%; Score 250.8; DB 28; Length 930;
 Best Local Similarity 65.1%; Pred. No. 3.6e-38;
 Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4;
 1343 TTGAGTTCATGTTGCTTCATCAATGATTTTGTACCCCTGAGCATTTGTCGAATTAATAC 1402
 920 TTGGTTTCAACCTTAACCTTCTTGTGTTACTTGCTGACGTCAAGCTCAAGTAATAC 861
 1403 CCTTGAAGGTTTGAATGTTTCGATGCGACATGATACATTAATCTTCCAGGTGTCACG 1462
 860 TCTGAGAGGTTGATGTTTGTGATGACAGATACATTAATCTTCCAGGTGTCACG 801
 1463 CGGCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1522
 800 TGGCCATCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 743
 1523 CTCTGATTCGTCACCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1582
 742 AACAAAAATCTATCTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 683
 1583 GATATTCATTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1642
 682 ACAATTTTACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 623
 1643 AAGAAATTAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1702
 622 AGGAATTAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 563
 1703 ATGATTAAGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1762
 562 ACGATTAAGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 510
 1763 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1822
 509 AGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 459
 1823 CTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1882
 458 ATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
 1883 TATTTTCTTCTAGTTTGTCTGATGATGATGATGATGATGATGATGATGATGATG 1942
 418 TATTTTCTTCTAGTTTGTCTGATGATGATGATGATGATGATGATGATGATGATG 376
 1943 ATTTTGAATTTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 2002
 375 ATTTTGAATTTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 316
 2003 TTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2050
 315 TTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 268

RESULT 2
 CG882826/c 985 bp DNA linear GSS 02-DEC-2003
 LOCUS ZMMB0492B17f ZMMBB (HindIII) Zea mays subsp. mays genomic clone
 DEFINITION ZMMB0492B17 5', genomic survey sequence.
 ACCESSION CG882826
 VERSION CG882826.1 GI:38613949

KEYWORDS
 SOURCE GSS
 ORGANISM Zea mays subsp. mays (maize)
 Zea mays subsp. mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 985)
 Bhatti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
 Zohovetz,V., Fuks,G., Yu,Y., Wang,R. and Messing,J.
 Sequencing of the maize genome at FGI (2003c)
 Unpublished (2003)
 TITLE
 JOURNAL
 COMMENT
 Dr. Joachim Messing's lab
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
 University
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 Tel: 732 445 3801
 Fax: 732 445 5735
 Email: bhatti@waksman.rutgers.edu
 Seq primer: 17
 Class: BAC ends
 High quality sequence start: 124.
 Location/Qualifiers
 1. 985
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 /mol_type="genomic DNA"
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 /note="Vector: pCUG1; Site_1: HindIII; Site_2: HindIII"

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 Query Match 9.0%; Score 183.8; DB 29; Length 985;
 Best Local Similarity 71.0%; Pred. No. 2.6e-25;
 Matches 306; Conservative 0; Mismatches 107; Indels 18; Gaps 4;
 1 CGAAGATTAATTCATATCTAATTTTAAAGATG-AGTGTGCGAAGATTTAAAGCT 59
 790 CAAAGATTAATTCATATCTAATTTTAAAGATG-AGTGTGCGAAGATTTAAAGCT 731
 60 TGGATTAATTCATATCTAATTTTAAAGATG-AGTGTGCGAAGATTTAAAGCT 119
 730 TGGATTAATTCATATCTAATTTTAAAGATG-AGTGTGCGAAGATTTAAAGCT 671
 120 GTATTCACA-----CAATCATTTTTCCTGATAC---ACTCTGACCAT 163
 670 GTATTCACAATTCATATCTAATTTTAAAGATG-AGTGTGCGAAGATTTAAAGCT 611
 164 TGGAGCTTAATTCATATCTAATTTTAAAGATG-AGTGTGCGAAGATTTAAAGCT 222
 610 CTGAAATCTGCTTCTAATGCTTTGTAACAAAGAGATCTGAATCGCCATTA 551
 223 TGAATTAATTCATATCTAATTTTAAAGATG-AGTGTGCGAAGATTTAAAGCT 282
 550 TTTCGAGCCATATTAACATCAATTTTAAAGATG-AGTGTGCGAAGATTTAAAGCT 491
 283 TGTTCAGGTATCATGATTTTAAAGATG-AGTGTGCGAAGATTTAAAGCT 342
 490 ATTTTCAGGTATCATGATTTTAAAGATG-AGTGTGCGAAGATTTAAAGCT 431
 343 GACTTAAATTCCTTGAATCGATGATGATGATGATGATGATGATGATGATGATGAT 402
 430 GACTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 371
 403 GTTCATAGATA 413
 370 GTTCATAGATA 360

RESULT 3
 CG882826/c 985 bp DNA linear GSS 02-DEC-2003
 LOCUS ZMMB0492B17f ZMMBB (HindIII) Zea mays subsp. mays genomic clone
 DEFINITION ZMMB0492B17 5', genomic survey sequence.
 ACCESSION CG882826
 VERSION CG882826.1 GI:38613949


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Db      200 -----GTATTAGATTCTTACTGTCTC 219
QY      1623 AAACGCAGATGCTGGGCTTGAGAAATPAAATTGATGGATTGATGATTTGGATTGATGAGGGGTAC 1682
Db      220 AAACGCAGATGCTGGGCTTGAGAAATPAAATTGATGGATTGATGATTTGGATTGATGAGGGGTAC 279
QY      1683 CTCGATATGTATCTACCACTGGATTACCAAGTAA 1717
Db      280 TTCATATATGATPACTCCACATGATTTACAAATGAC 314

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RESULT	5
LOCUS	BU967331
DEFINITION	H803P08 BC Hordeum vulgare subsp. vulgare CDNA clone HB03P08
ACCESSION	BU967331
VERSION	GI:24218124
KEYWORDS	EST.
SOURCE	Hordeum vulgare subsp. vulgare
ORGANISM	Hordeum vulgare subsp. vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum. 1 (bases 1 to 537) Rachunk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U. Barley ESTs from developing seeds Unpublished (2002) Contact: Stein Nils Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstr. 3, 06466, Gatersleben, Germany Tel.: 039482-5522 Fax: 039482-5595 Email: stein@ipk-gatersleben.de Insert length: 537 Std Error: 0.00 Plate: 3 row: P column: 8 Seq primer: MJ3rev.

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FEATURES
source
Location/Qualifiers
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/dev_stage="8-15 DAP (days after pollination)"
/lab_host="X110-Gold"
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/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); developing carpovels, 8-15 DAP (days after pollination) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

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ORIGIN	Query Match	Best Local Similarity	Score	DB 13	Length	537
			6.8%;			
			71.9%;			
			Pred. No. 1e-16;			
	Matches	241;	Conservative	0;	Mismatches	6;
					Indels	88;
					Gaps	1
QY	1383	AGTCATTGCTCAAAATATATACCCCTTGACGGTTTGAATGCTTGCATGACATGATAACAT	144			
DB	29	AGTCATTGCTCAAAATATATACCCCTTGACGGTTTGAATGCTTGCATGACATGATAACAT	88			
QY	1443	TACTTCCACGGTGGTCCACGCGGCCCATTCATTTGGATGTGGATTTCTGCTATTCAACTAT	150			
DB	89	TACTTCCACGGTGGTCCACGCGGCCCATTCATTTGGATGTGGATTTCTGCTATTCAACTAT	148			

QY	1503	GGAGATTGGGAAGATATATGACTCTGACTCTGTGCACATATTTGGCTAACGTTCCAGTT	1562
Db	149	GGAGATTGGGA-----	160
QY	1563	AATCTGTTTACACATGTGATATCTATTCATTATGACAGATATGAGATTCCTACTGTC	1622
Db	161	-----GATTAAGATCTTACGTC	180
QY	1623	AAACGCGAGTGGTGGCTTGAAGATATTAAGTTGATGATTCGATTTGTGGGGTGAC	1682
Db	181	AAACGCGAGTGGTGGCTTGAAGATATTAAGTTGATGATTTGATTTGATGGGGTGAC	240
QY	1683	CTCCATGATGTATATCTCACCATGGATTACAAGTAA	1717
Db	241	TTCCATGATGTATATCTCACCATGGATTACAAGTAA	275

RESULT	6
LOCUS	BQ245037
DEFINITION	BQ245037 TAEI5032A02R TAb15 Triticum aestivum cDNA clone TAEI5032A02R, mRNA
ACCESSION	BQ245037
VERSION	BQ245037.1
KEYWORDS	GI:20440913
SOURCE	EST.
ORGANISM	Triticum aestivum (bread wheat)
AUTHORS	Triticum aestivum
TITLE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.
JOURNAL	1 (bases 1 to 476) Cloutier,S. wheat functional genomics - Glenea developing seeds cDNA libraries Unpublished (2002)
COMMENT	Contact: Dr. Sylvie Cloutier Crop Development Centre University of Guelph, Ontario, Canada

```

FEATURES
Source
    Email: sclouvier@agr.gc.ca
    Cereia_research@century.net, AgResearch@century.net
    195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
    Tel: (204) 983-2340
    Fax: (204) 983-4604
    Seq primer: M13 Reverse.
    Location/Qualifiers
        1..476
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            of cultivar Glenlea 15 days post-anthesis"

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ORIGIN	Query Match	6.5%	Score 134	DB 13	length 476	
	Best Local Similarity	96.5%	Pred No. 1,le-15			
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QY	1909	TTCTAGATGACATTACTGCGAACAATGCGCAATATTTTGGATTGGCTACTGATGTTGAT	196			
Db	142	TTACAAATGACATTACTGCGAACAATGCGCAATATTTTGGATTGGCTACTGATGTTGAT	201			
QY	1969	GCGGTAGTTACTTGATGCTGCTCAACGATCTTAATTCATGAGCTTTATCCTGATGCTGTA	202			
Db	202	GCGGTAGTTACTTGATGCTGCTCAACGATCTTAATTCATGAGCTTTATCCTGATGCTGTA	261			

QY 2029 TCCATTGGTGAAGATGTAGTG 2050
DB 262 TCCATTGGTGAAGATGTAGTG 283

RESULT 7
LOCUS BU986646
DEFINITION HF12102r HF Hordeum vulgare subsp. vulgare cDNA clone HF12102
ACCESSION BU986646 623 bp mRNA linear EST 22-OCT-2002
VERSION BU986646
KEYWORDS 5-PRIME, mRNA sequence.
SOURCE BU986646.1 GI:24237592
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 623)
AUTHORS Radchuk V., Zhang H., Weschke W., Potokina E. and Mabus U.
TITLE Barley ESTs from developing seeds
JOURNAL Unpublished (2002)
COMMENT Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 623 Std Error: 0.00
Plate: 12 row: 1 column: 2
Seq primer: M13rev.
Location/Qualifiers
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/db_xref="taxon:112509"
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/note="Vector: pBluescript SK+, Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); developing caryopsis, 16-25 DAF (days after flowering) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable. Average insert size is 940 bp"

ORIGIN
Query Match 6.5%; Score 134; DB 13; Length 623;
Best Local Similarity 96.5%; Pred. No. 1.1e-15;
Matches 137; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DB 1383 AGTCATTCGCAATAATACCTTGACGGTTGATGTTTCGATGGCACTGATACAT 1442
DB 463 AGTCATTCGCAATAATACCTTGACGGTTGATGTTTCGATGGCACTGATACAT 522
QY 1443 TACTTCACGCGTGTCCACGCGGCATCATTTGGATGTTCTGTTTCAACTAT 1502
DB 523 TACTTCACGCGTGTCCACGCGGCATCATTTGGATGTTCTGTTTCAACTAT 582
QY 1503 GGGAGTTGGAGTATGTAGCT 1524

DB 583 GGGAGTTGGAGTATGTAGAT 604

RESULT 8
LOCUS AQ576669/c
DEFINITION nbxb008901r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb008901r, genomic survey sequence.
ACCESSION AQ576669 610 bp DNA linear GSS 02-JUN-1999
VERSION AQ576669
KEYWORDS AQ576669.1 GI:4977154
SOURCE GSS.
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriocaridaceae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 610)
AUTHORS Wang R.A. and Dean R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Wang RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7268
Fax: 864 656 4293
Email: twing@clemson.edu
Seq primer: GGAACACGATGACCATG
Class: BAC ends
High quality sequence stop: 442.
Location/Qualifiers
1..610
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/mol_type="genomic DNA"
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/db_xref="taxon:39947"
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/note="Vector: pBelBAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

ORIGIN
Query Match 6.5%; Score 133.2; DB 28; Length 610;
Best Local Similarity 59.1%; Pred. No. 1.5e-15;
Matches 344; Conservative 0; Mismatches 168; Indels 70; Gaps 4;

QY 1478 GTGGGATTCGCTATATCACTATGGAGTTGGAGTA-----TGTAGCTCTGA 1528
DB 610 GTGGGATTCGCTATATCACTATGGAGTTGGAGTAAGAAACACCTTAATCCTCT 551
QY 1529 CTTCTGCACCATATTTGGCTAACTGTTCCGTTATATCTGTTCTTACACATGTTGATAT 1588

Db 550 TTCCCTTACCAAGATGATCATTTATTCATATGATTCATATCTCTATGTGTGCGCAACATTT 491
QY 1589 CATTCCTTATGACGATGATGAGATTTCTTACTGTCMAAGCGAGATGGGCTTGAAGAT 1648
Db 490 TTTCTCTTATACAGGTTCTTACGATTTCTACTATCCATGCAAGATGGTGGCTGAGAGT 431
QY 1649 ATTAAGTTGATGATTTGATTTGATGGGATGAGCTTCATGATGATATCACTCAGAT 1708
Db 430 ATTAAGTTGATGATTTGATTTGATGGGATGAGCTTCATGATGATATCACTCAGAT 371
QY 1709 TACAGTAACTGATCAAGTGGTTTCACTTCTTTTAAAGGACATGAAACATTTGCTATG 1768
Db 370 TACAAAGTA--TATGCTCTCTTTTCACTTACTTATCTTCACTACCTCTTATATATGATG 313
QY 1769 CATCATTAACATGATATCATGATCAAGACTTGTGCTACGAGATCTTAAATAGTCCCTAGTA 1828
Db 312 GGGTCMAACCTACGAGTGGCTA-----TCTGTTACATTTCAATTTATTTTGGCTCAT 259
QY 1829 TGCTTGATCAATTTTACCTGATGATGATGATGAGATTTGAAGTATATTTATTTT 1888
Db 258 ACCT-----TTA 252
QY 1889 CTTCCTTAAGTTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1948
Db 251 TCTTATGATTCACCCCTCTATTTTATGATGATGATGATGATGATGATGATGATGATGATG 192
QY 1949 GATTCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2008
Db 191 GATTCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 132
QY 2009 GACTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2050
Db 131 GACTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 90

RESULT 9
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LOCUS G118.114J06F010718 G118 Triticum aestivum cDNA clone G118114J06,
DEFINITION mRNA sequence.
ACCESSION CD890409
VERSION CD890409.1 GI:32659746
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 621)
AUTHORS Genoplante.
TITLES Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante

Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme "Genoplante" (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).
Location/Qualifiers
1..621
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pollination)"
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FEATURES
source

ORIGIN

Best Local Similarity 95.8%; Pred. No. 2.2e-15;
Matches 136; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1909 TTCTGATGACATTTACTGAGGACATGAGGAAATATTTGATTTGCTACTGATGAT 1968
Db 96 TTACAAAGACATTTACTGAGGACATGAGGAAATATTTGATTTGCTACTGATGAT 135
QY 1969 GCGGTAGTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2028
Db 156 GCGGTAGTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 215
QY 2029 TCCATGTTGAAAGATGATGATG 2050
Db 216 TCCATGTTGAAAGATGATGATG 237

RESULT 10
AV939010 678 bp mRNA linear EST 18-JAN-2002
LOCUS AV939010 K. Sato unpublished cDNA library, strain H602 adult,
DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
cDNA clone bah20e24 5', mRNA sequence.
ACCESSION AV939010.1 GI:18234807
VERSION AV939010.1
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 678)
AUTHORS Sato, K., Saitoh, D. and Takeda, K.
TITLES Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsuhin@genes.nig.ac.jp.
Location/Qualifiers
1..678
/organism="Hordeum vulgare subsp. spontaneum"
/mol_type="mRNA"
/strain="H602"
/sub_species="spontaneum"
/db_xref="taxon:77009"
/clone="bah20e24"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/clone_1b="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"

ORIGIN

Query Match 6.1%; Score 125.8; DB 9; Length 678;
Best Local Similarity 84.0%; Pred. No. 3.9e-14;
Matches 142; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 280 CTTGTTCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 339
Db 495 GCGAGCTTTGGGTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 554
QY 340 GAGACCTTAATCCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 359
Db 555 GAGACCTTAATCCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 614
QY 400 ATTGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 448
Db 615 ATTGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 663

BU970967 411 bp mRNA linear EST 22-OCT-2002
 LOCUS HB16D15R BC Hordeum vulgare subsp. vulgare cDNA clone HB16D15
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION BU970967
 VERSION BU970967.1 GI:24221760
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 411)
 AUTHORS Radchuk,V., Zhang,H., Weschke,W., Potokina,E. and Wobus,U.
 TITLE Barley ESTs from developing seeds
 JOURNAL Unpublished (2002)
 COMMENT Contact: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert Length: 411 Std Error: 0.00
 Plate: 16 row: D column: 15
 Seq primer: M13rev.
 Location/Qualifiers
 1..411
 /organism="Hordeum vulgare subsp. vulgare"
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 /db_xref="taxon:112509"
 /clone="HB16D15"
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 /dev_stage="8-15 DAP (days after pollination)"
 /lab_host="XLI0-Gold"
 /clone_1lb="BC"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); developing caryopsis, 8-15 DAP (days after pollination) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/White selection for recombinants is not 100% reliable."

ORIGIN
 Query Match 6.1%; Score 124.4; DB 13; Length 411;
 Best Local Similarity 92.3%; Pred. No. 8.1e-14;
 Matches 131; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 1909 TTCTAGATGACATTACTGCGGAACTATTTGGATTGCTACTATGTTGAT 1968
 DB 144 TTACAAATGACATTACTGCGGAACTATTTGGATTGCTACTATGTTGAT 203
 QY 1969 GCGGAGTTTACTGATGCTGTCACATCTAATTCATGAGTCTTATCTGATGCTGA 2028
 DB 204 GCGGAGTTTACTGATGCTGTCACATCTAATTCATGAGTCTTATCTGATGCTGA 263
 QY 2029 TCCATTGGTGAAGATGTAAGTG 2050
 DB 264 TCCATTGGTGAAGATGTCAGCG 285
 RESULT 12
 CA292638 618 bp mRNA linear EST 26-SEP-2003
 LOCUS SCRF18025G06.g FL8 Saccharum officinarum cDNA clone SCRF18025G06
 DEFINITION 5', mRNA sequence.

VERSION CA292638.1 GI:36051621
 KEYWORDS EST.
 SOURCE Saccharum officinarum
 ORGANISM Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogonaceae; Saccharum.
 REFERENCE 1 (bases 1 to 618)
 AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
 TITLE The libraries that made SUCEST
 JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 COMMENT Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: parruda@unicamp.br
 Clone distribution: clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fcav.unesp.br
 Plate: 025 row: G column: 06
 Seq primer: T7 Promoter Primer.
 Location/Qualifiers
 1..618
 /organism="Saccharum officinarum"
 /mol_type="mRNA"
 /db_xref="taxon:4547"
 /clone="SCRF18025G06"
 /lab_host="DH10B"
 /clone_1lb="FL8"
 /note="Organ: Developing inflorescence and rachis (10cm-long); Vector: pSPORT1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [developing inflorescence and rachis (10cm-long)]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sapharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at
 http://sucest.lad.ic.unicamp.br/public"

ORIGIN
 Query Match 6.0%; Score 123.2; DB 14; Length 618;
 Best Local Similarity 91.0%; Pred. No. 1.3e-13;
 Matches 131; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 1383 AGTATTCGCAATTAATTAACCTTGAGCGTTGATGTTGGATGGACGATACACAT 1442
 DB 218 AGTATTCGCAATTAATTAACCTTGAGCGTTGATGTTGGATGGACGATACACAT 277
 QY 1443 TACTTCACGAGTGTCCACGCGGCATCATTTGATGAGATTCTGCTATTCACATAT 1502
 DB 278 TACTTCACGAGTGTCCACGCGGCATCATTTGATGAGATTCTGCTATTCACATAT 337
 QY 1503 GCGAGTTGGGAAGTATGAGCTCT 1526
 DB 338 GCGAGTTGGGAAGTATGAGATAT 361
 RESULT 13
 CA202517 650 bp mRNA linear EST 25-SEP-2003
 LOCUS SCRF11027B04.g FL1 Saccharum officinarum cDNA clone SCRF11027B04
 DEFINITION 5', mRNA sequence.
 ACCESSION CA202517
 VERSION CA202517.1 GI:35237862
 KEYWORDS EST.
 SOURCE Saccharum officinarum
 ORGANISM Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

REFERENCE 1 (bases 1 to 650)
 AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
 TITLE The libraries that made SUCEST
 JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 COMMENT Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: parud@unicamp.br
 Clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fcav.unesp.br
 Plate: 027 row: B column: 04
 Seq primer: T7 Promoter Primer.
 Location/Qualifiers
 1..650
 /organism="Saccharum officinarum"
 /mol_type="mRNA"
 /db_xref="taxon:4547"
 /clone="SCRFPL1027804"
 /lab_host="DH103"
 /clone_lib="FL1"
 /note="Organ: Inflorescence at beginning of development (1cm-long); Vector: pSPORT; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from Inflorescence at beginning of development (1cm-long). cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://succest.lad.ic.unicamp.br/public"

ORIGIN
 Query Match 6.0%; Score 123.2; DB 14; Length 650;
 Best Local Similarity 91.0%; Pred. No. 1.2e-13;
 Matches 131; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

CY 1383 AGTCATTCGTCAAATTAATACCCCTTGAGCGTTGATGGTTCGATGGACATGATACAT 1442
 DB 188 AGTCATGATCAATTAATACCTTGAGCGTTGATGGTTCGATGGACATGATACAT 247

CY 1443 TACTTCCAGCGGTGTCACGGCCCATCATGATGGATTCGCTCATTAACAT 1502
 DB 248 TACTTCCATGATGTCACGGCCCATCATGATGGATTCGCTCATTAACAT 307

CY 1503 GGGAGTTGGAGATGATGACTCT 1526
 DB 308 GGGAGTTGGAGATGATGACTCT 331

RESULT 14
 AY109521 2766 bp mRNA linear HTC 17-OCT-2002
 LOCUS AY109521
 DEFINITION Zea mays CL1245_1 mRNA sequence.
 ACCESSION AY109521
 VERSION AY109521.1 GI:21213273
 KEYWORDS HTC.
 ORGANISM Zea mays
 SOURCE Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 2766)
 AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
 TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes
 JOURNAL Unpublished (2002)

REFERENCE 2 (bases 1 to 2766)
 AUTHORS Coe,E.H.
 TITLE Direct Submission
 JOURNAL Submitted (25-Apr-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
 COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZMDB and may be found by BLAST searching at MSU, maizegap.org; ZMDB, www.zmdb.iastate.edu; TRGR, www.trgr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZMDB: www.zmdb.iastate.edu.
 Location/Qualifiers
 1..2766
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="taxon:4577"
 /db_xref="maizeDB:630161"
 /clone_lib="Maize Mapping Project/Dupont Consensus Library"
 /note="This sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN
 Query Match 6.0%; Score 122.2; DB 11; Length 2766;
 Best Local Similarity 88.1%; Pred. No. 1.4e-13;
 Matches 133; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

CY 1393 AGTCATTCGTCAAATTAATACCCCTTGAGCGTTGATGGTTCGATGGACATGATACAT 1442
 DB 1172 AGTCATTCATCAATTAATACCTTGATGGTTCGATGGTTCGATGGACATGATACAT 1231

CY 1443 TACTTCCAGCGGTGTCACGGCCCATCATGATGGATTCGCTCATTAACAT 1502
 DB 1232 TACTTCCATGATGTCACGGCCCATCATGATGGATTCGCTCATTAACAT 1291

CY 1503 GGGAGTTGGAGATGATGACTCTGACTTCT 1533
 DB 1292 GGGAGTTGGAGATGATGACTCTGACTTCT 1322

RESULT 15
 BM660711 399 bp mRNA linear EST 27-FEB-2002
 LOCUS BM660711
 DEFINITION 952041807.xl 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea mays cDNA, mRNA sequence.
 ACCESSION BM660711
 VERSION BM660711.1 GI:18963932
 KEYWORDS EST.
 ORGANISM Zea mays
 SOURCE Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 399)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 952041 row: B column: 07.
 Location/Qualifiers
 1..399

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/organism="Zea mays"  
/mol_type="mRNA"  
/cultivar="BMS (Black Mexican Sweet)"  
/db_xref="taxon:4577"  
/tissue_type="suspension culture"  
/dev_stage="mixed logarithmic and stationary growth  
phases"  
/lab_host="DH10B"  
/clone_id="952 - BMS tissue from Walbot lab (reduced  
RNA)"  
/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and Universal Riboclone cDNA Synthesis System  
(Promega). cDNA was synthesized using both random and  
oligo(dT) primers in separate reactions and equipped with  
EcoRI adaptors. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-directionally cloned  
into EcoRI-digested pUC19 vector. Blue/white selection on  
carbenicillin-containing plates was used to recover  
positive clones."
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ORIGIN

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Query Match      5.9%; Score 121.6; DB 12; Length 399;  
Best Local Similarity 82.7%; Pred. No. 2.8e-13;  
Matches 139; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
  
QY      1383 AGTCATTGTCGAATATATACCCCTTGACGGTTGAATGATTGCGATGGCACTGATACACAT 1442  
          |||||  
DB      224 AGTCATTGTCGAATATATACCCCTTGATGGTTGAATGATTGATGGCACTGATACACAT 283  
          |||||  
  
QY      1443 TACTTCCACGGTGGTCCACGCGGCCCATCTTGATGTGGGATTCGCTCTATTCACCTAT 1502  
          |||||  
DB      284 TACTTCCATGGGTGCCACGCGGCCCATCTTGATGTGGGATTCGCTCTATTCACCTAT 343  
          |||||  
  
QY      1503 GGGAGTTGGGAAGTATGTAGCTGTGACTCTGTGCACCATATTTGGCTA 1550  
          |||||  
DB      344 GGGAGTTGGGAAGTTTGGAGATTCTCTACTGTCAATGCCAGATGGCGA 391  
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Search completed: April 10, 2004, 14:06:33
Job time : 5423.32 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 01:54:35 ; Search time 5268.31 seconds

(without alignments)
11057.263 Million cell updates/sec

Title: US-09-508-377-10_COPY_10120_11463

Perfect score: 1344

Sequence: 1 ttgataatcgcgtgctgcga.....tcgcctcaacgtgaaatcc 1344

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

- 1: gb_ba:*
- 2: gb_hcg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_scs:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vt:*
- 15: gb_da:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_scs:*
- 28: em_un:*
- 29: em_vt:*
- 30: em_hcg_hum:*
- 31: em_hcg_inv:*
- 32: em_hcg_other:*
- 33: em_hcg_mus:*
- 34: em_hcg_pln:*
- 35: em_hcg_rod:*
- 36: em_hcg_mam:*
- 37: em_hcg_vrt:*
- 38: em_sy:*
- 39: em_hgo_hum:*
- 40: em_hgo_mus:*
- 41: em_hgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1344	100.0	11463	6 AX031271
2	1344	100.0	11475	8 AF38431
3	370	27.5	1119	6 AX756279
4	370	27.5	2853	6 AR340173
5	370	27.5	2853	6 TA06376
6	361.6	26.9	2970	8 AF286319
7	360.6	26.8	2726	8 AF38432
8	360	26.8	2970	8 TMSB2
9	263.6	19.6	2554	8 AF064560
10	158.8	11.8	2549	8 BT008928
11	132.4	9.9	1292	8 AY235404
12	132.4	9.9	1373	8 AY235395
13	132.4	9.9	1374	8 AY235421
14	132.4	9.9	1382	8 AY235405
15	132.4	9.9	1393	8 AY235396
16	132.4	9.9	1393	8 AY235399
17	132.4	9.9	1394	8 AY235397
18	132.4	9.9	1394	8 AY235407
19	132.4	9.9	1394	8 AY235409
20	132.4	9.9	1394	8 AY235410
21	132.4	9.9	1394	8 AY235415
22	132.4	9.9	1397	8 AY235394
23	132.4	9.9	1399	8 AY235398
24	132.4	9.9	1399	8 AY235408
25	132.4	9.9	1399	8 AY235416
26	132.4	9.9	1399	8 AY235418
27	132.4	9.9	1399	8 AY235419
28	132.4	9.9	1399	8 AY235422
29	132.4	9.9	1400	8 AY235400
30	132.4	9.9	1400	8 AY235401
31	132.4	9.9	1400	8 AY235402
32	132.4	9.9	1400	8 AY235403
33	132.4	9.9	1400	8 AY235411
34	132.4	9.9	1400	8 AY235412
35	132.4	9.9	1400	8 AY235413
36	132.4	9.9	1400	8 AY235414
37	132.4	9.9	1400	8 AY235420
38	132.4	9.9	1401	8 AY235417
39	132.4	9.9	1618	8 AF072725
40	132.4	9.9	23449	8 AF072725
41	125.6	9.3	2446	6 AR427891
42	125.6	9.3	2795	8 ZMU65948
43	124.4	9.3	2307	6 AX755372
44	123.4	9.2	2304	6 AX755783
45	123.4	9.2	2364	6 E14724

ALIGNMENTS

RESULT 1
AX031271
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

AX031271 11463 bp DNA linear PAT 20-SEP-2000
Sequence 10 from Patent WO9914314.
AX031271.1 GI:10278603
Aegilops tauschii
Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Aegilops.
1
Li, Z., Morell, M. and Rahman, S.
Regulation of gene expression in plants

JOURNAL Patent: WO 9914314-A 10 25-MAR-1999;
GOODMAN FIDLER LTD (AU) ; LI ZHONGYI (AU) ; MORELL MATTHEW (AU) ;
RAHMAN SADIQUR (AU) ; UNIV AUSTRALIAN (AU) ; COMM SCIENT IND RES
ORG (AU) ; GROUPE LIMAGRAIN PACIFIC PTY L (AU)
Location/Qualifiers
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1. 11463
/organism="Aegilops tauschii"
/mol_type="unassigned DNA"
/db_xref="taxon:37682"
/issue_type="ENDOSPERM"
misc_feature
1. 11463
/product="COMPLETE SEQUENCE OF THE STARCH BRANCHING ENZYME
II GENE"
ORIGIN
Query Match 100.0%; Score 1344; DB 6; Length 11463;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGATATTCGTGTGATGCAAGAGTTGCATCAGGCAATGACGATCTTGAGAAAAATATG 60
DB 10120 TTGATATTCGTGTGATGCAAGAGTTGCATCAGGCAATGACGATCTTGAGAAAAATATG 10179
QY 61 GGGTATGTCCTGCTGTTGCTTTGTTGTCATPACAAAGTCACAGTTTAAAGTCTCTC 120
DB 10180 GGGTATGTCCTGCTGTTGCTTTGTTGTCATPACAAAGTCACAGTTTAAAGTCTCTC 10239
QY 121 AAGTGTAAAAAAGTGTAGATTAATTCCTGTANTGATGATAAAGTGTGCAAGAGCG 180
DB 10240 AAGTGTAAAAAAGTGTAGATTAATTCCTGTANTGATGATAAAGTGTGCAAGAGCG 10299
QY 181 AAGTGTAAATGCTTTTACCAAAAAGTATTTTCTTAAGTCTGTGTATGATACATATAC 240
DB 10300 AAGTGTAAATGCTTTTACCAAAAAGTATTTTCTTAAGTCTGTGTATGATACATATAC 10359
QY 241 CAGACCTGACAATGTACTGCAAGTTTATGACATGTCAGCAACATATGTTTCAAGGAAC 300
DB 10360 CAGACCTGACAATGTACTGCAAGTTTATGACATGTCAGCAACATATGTTTCAAGGAAC 10419
QY 301 ATGAGAGAGATTAAGTATCATCTCTCAAAAAGAGAGATTTGATTTGTTTCAACTTC 360
DB 10420 ATGAGAGAGATTAAGTATCATCTCTCAAAAAGAGAGATTTGATTTGTTTCAACTTC 10479
QY 361 ACTGAGCAATAGCTTTTGTGACTACCGGTGGGTGTTCCAAAGCTGGGAATGCAAG 420
DB 10480 ACTGAGCAATAGCTTTTGTGACTACCGGTGGGTGTTCCAAAGCTGGGAATGCAAG 10539
QY 421 TAGGCTTGCTTTTCAATGTCACCCCTTCAACAGTAAAGGTTAGGGGGCTTTCAACT 480
DB 10540 TAGGCTTGCTTTTCAATGTCACCCCTTCAACAGTAAAGGTTAGGGGGCTTTCAACT 10599
QY 481 TTAAATTCACATGATAGATTTGTTGTCGTGACGATCATCAATATTAAGATAGGTA 540
DB 10600 TTAAATTCACATGATAGATTTGTTGTCGTGACGATCATCAATATTAAGATAGGTA 10659
QY 541 ATTGTGAAGAAAAAATTGCTGAGCTGTTGATGACCATGGAAGGTTGTTCTTAACAG 600
DB 10660 ATTGTGAAGAAAAAATTGCTGAGCTGTTGATGACCATGGAAGGTTGTTCTTAACAG 10719
QY 601 CCGCGAAGCACAATCAATCATATATATCACTTAAGGTTGTTGATCTTTATG 660
DB 10720 CCGCGAAGCACAATCAATCATATATATCACTTAAGGTTGTTGATCTTTATG 10779
QY 661 CTCAGTTGACCTGGTCTAATACAGATATTTCCGAATCTACCCATACCATCTTAC 720
DB 10780 CTCAGTTGACCTGGTCTAATACAGATATTTCCGAATCTACCCATACCATCTTAC 10839
QY 721 AGTTTGAAGACCCCATTTTGAACAATGGCTGGGTTTGTATGTTGACAGTTTCT 780
DB 10840 AGTTTGAAGACCCCATTTTGAACAATGGCTGGGTTTGTATGTTGACAGTTTCT 10899
QY 781 GCATTTCTTAATAGGTGGCTTGACCTGACGATGACATCTTTGGTGAATTCAGAG 840

DB 10900 GCATTTCTTAATAGGTGGCTTGACCTGACGATGACATCTTTGGTGAATTCAGAG 10959
QY 841 GCTTGATCATGATGTCGACTACTTACAAACGCTAAGTCTGAGCTCAAGGTCATGACT 900
DB 10960 GCTTGATCATGATGTCGACTACTTACAAACGCTAAGTCTGAGCTCAAGGTCATGACT 11019
QY 901 GCTCTTGACCTCAACGCTTACAAATCTGAATCACTCCCAATTTGCTGATGGCCTTGAC 960
DB 11020 GCTCTTGACCTCAACGCTTACAAATCTGAATCACTCCCAATTTGCTGATGGCCTTGAC 11079
QY 961 GAACATCCGACATGACAACAGCGCGCTTTCTGCGTGTACACTCCGACAGAACTGCG 1020
DB 11080 GAACATCCGACATGACAACAGCGCGCTTTCTGCGTGTACACTCCGACAGAACTGCG 11139
QY 1021 GTGCTGTATGCCCTTACAGATTAAGAACCAAGCAGCGCTTTGTTACAGGCAAGAGAA 1080
DB 11140 GTGCTGTATGCCCTTACAGATTAAGAACCAAGCAGCGCTTTGTTACAGGCAAGAGAA 11199
QY 1081 CTCACAGAGCTCGTGTATGTCGAGGAGACAGCGGCAACGCGGAGGCTGCTCCAG 1140
DB 11200 CTCACAGAGCTCGTGTATGTCGAGGAGACAGCGGCAACGCGGAGGCTGCTCCAG 11259
QY 1141 CGCCTGACTGCGGAGGAGATCGTGCCTCTTCCCAAGATGCCAGAGAGAGATGATAG 1200
DB 11260 CGCCTGACTGCGGAGGAGATCGTGCCTCTTCCCAAGATGCCAGAGAGAGATGATAG 11319
QY 1201 GTAGCTTGTGTGAGCGCTCGAAGAAATGACCGGCTGGGTGTTGTTGCTGCA 1260
DB 11320 GTAGCTTGTGTGAGCGCTCGAAGAAATGACCGGCTGGGTGTTGTTGCTGCA 11379
QY 1261 CTGAACCTCCCTCCATCTTGCACATTCGCGGTGTTTGTGATATATAATAATG 1320
DB 11380 CTGAACCTCCCTCCATCTTGCACATTCGCGGTGTTTGTGATATATAATAATG 11439
QY 1321 CCGGTGCGCTCAAGTGAATAATCC 1344
DB 11440 CCGGTGCGCTCAAGTGAATAATCC 11463
RESULT 2
AF338431 11475 bp DNA linear PLN 27-MAR-2001
LOCUS Aegilops tauschii starch branching enzyme IIa gene, complete cds.
DEFINITION
AF338431
ACCESSION
AF338431.1 GI:13447949
KEYWORDS
ORGANISM
Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Aegilops.
REFERENCE
1 (bases 1 to 11475)
Rahman,S., Regina,A., Li,Z., Sharon,A. and Morell,M.K.
Kosar-Hashemi,B., Abrahams,S. and Morell,M.K.
Comparison of starch-branching enzyme genes reveals evolutionary
relationships among isoforms. Characterization of a gene for
starch-branching enzyme IIa from the wheat genome donor Aegilops
tauschii
JOURNAL Plant Physiol. 125 (3), 1314-1324 (2001)
MEDLINE 21140316
PUBMED 11244112
REFERENCE 2 (bases 1 to 11475)
Rahman,S., Regina,A., Li,Z., Sharon,A. and Morell,M.K.
Direct Submission
TITLE
JOURNAL Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Rose,
Canberra, ACT 2601, Australia
FEATURES
source
1. 11475
/organism="Aegilops tauschii"
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/chromosome="2"
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4418..4939,5115..5234,6209..6338,6427..6537,6739..6867,
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Join(1204..1136,1664..1761,2038..2279,2681..2779,
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4418..4939,5115..5234,6209..6338,6427..6537,6739..6867,
7447..7550,8392..8536,9556..9703,9839..9939,10116..10193,
10395..10550,10928..11002,11092..11175)
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NARWLEBYKFDGFRPDGVTSMYTHHGLQMTFTGNGEYFGFATDVAVYMLVND
LHGLYDPAVSIQEDVSGMPTFCIPVDGQGFEDYRLHMAVADKMIILKQSDSMX
GIIVHILNRWLEKCVYAEASHDOLVGGKTIAPMDMDMTVFNALDRSTLDR
GALHMTIRLVLGEGEYLMNGEFGHEMTDPRGQTLITGVVLKPNNSYK
CRRPFLGDADPIRYRGMQSPDAMQHLKEKYGEMTSEHOVYSKHEDEKYLTKRD
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RRSFVSVPSTRAVYVALTE"

ORIGIN

Query Match 100.0%; Score 1344; DB 8; Length 11475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATCGTGTATGCAAGAGTTCGATCAGCAATGACATCTTGAGGAAAAATATG 60
Db 10132 TTGAATCGTGTATGCAAGAGTTCGATCAGCAATGACATCTTGAGGAAAAATATG 10191
QY 61 GGGTATGTCATCGTGTGCTTTGTCATPAACAAGTCACAGTTTAACGTACGTCTTC 120
Db 10192 GGGTATGTCATCGTGTGCTTTGTCATPAACAAGTCACAGTTTAACGTACGTCTTC 10251
QY 121 AAGTGTAAAAAAGTGTAAATTAATTCCTGTATGATGAGAAACGTGCCAAGGCGG 180
Db 10252 AAGTGTAAAAAAGTGTAAATTAATTCCTGTATGATGAGAAACGTGCCAAGGCGG 10311
QY 181 AGCTGAATGCTTTTACCAAAACATTTTCTTAAGTCTTGATATGATATATAC 240
Db 10312 AGCTGAATGCTTTTACCAAAACATTTTCTTAAGTCTTGATATGATATATAC 10371
QY 241 CAGCACTGACATGTAACTGCAAGTTATGACATCTGACACCAAGTATGTCACGGAAC 300
Db 10372 CAGCACTGACATGTAACTGCAAGTTATGACATCTGACACCAAGTATGTCACGGAAC 10431
QY 301 ATGAGAGAATAGTATGATCTCTCAAAAGAGAGATTGTTGTTTTCACACTTC 360
Db 10432 ATGAGAGAATAGTATGATCTCTCAAAAGAGAGATTGTTGTTTTCACACTTC 10491
QY 361 ACTGAGACATAGCTTTTGTGACTACCGTGTGGGTGTTCCAGCCTGGAGATACAAG 420
Db 10492 ACTGAGACATAGCTTTTGTGACTACCGTGTGGGTGTTCCAGCCTGGAGATACAAG 10551
QY 421 TATGCTTGCTTTTCAATGTCACCTTCACCAAGTAGGGTTAGTGGGGCTTTCAACT 480
Db 10552 TATGCTTGCTTTTCAATGTCACCTTCACCAAGTAGGGTTAGTGGGGCTTTCAACT 10611
QY 481 TTTAATTCACATGATAGAGTTGTTGGTGTGCAAGTATCATATATAAGATAGGGTA 540
Db 10612 TTTAATTCACATGATAGAGTTGTTGGTGTGCAAGTATCATATATAAGATAGGGTA 10671
QY 541 ATTGTAAAGAAAAAGATTGCTGACACTGTTGTAGCCATAGGAAGGTGTTCTTAACAG 600

Db 10672 ATTGTAAAGAAAAAGATTGCTGACACTGTTGTAGCCATAGGAAGTTGTTTAAACAG 10731
QY 601 CCCGAAACACATACCATTCATTCATATATCTAGTGTGTTCAATCTTATG 660
Db 10732 CCCGAAACACATACCATTCATTCATATATCTAGTGTGTTCAATCTTATG 10791
QY 661 CTCAGTTGACCTGGCTTAATCTAGTAACTATTTTCCGATCTACCCCTAACCTTACG 720
Db 10792 CTCAGTTGACCTGGCTTAATCTAGTAACTATTTTCCGATCTACCCCTAACCTTACG 10851
QY 721 AGTTTAAAGACCCCAATTTGACCAATTTGCTGGGTTTGTAGTTGACAGTTTCT 780
Db 10852 AGTTTAAAGACCCCAATTTGACCAATTTGCTGGGTTTGTAGTTGACAGTTTCT 10911
QY 781 GCTATTTCTTAATCAGTGGCTTGGACTCTGACATGACCTTTGTTGATTCAGCAG 840
Db 10912 GCTATTTCTTAATCAGTGGCTTGGACTCTGACATGACCTTTGTTGATTCAGCAG 10971
QY 841 GCTTATCATGATGTGCACTACTTCAACACCGTAACTGAGCTCAAGCTCACTTACT 900
Db 10972 GCTTATCATGATGTGCACTACTTCAACACCGTAACTGAGCTCAAGCTCACTTACT 11031
QY 901 GCTCTTGACTCAACTGCTTACAAATCTGAATCACTTCCCAATTTGCTGATGCCCTTCAG 960
Db 11032 GCTCTTGACTCAACTGCTTACAAATCTGAATCACTTCCCAATTTGCTGATGCCCTTCAG 11091
QY 961 GAACATCCGACATGACAAACAGCGCGGCTTCTCGGTGTACACTCCGACAGAACTGCG 1020
Db 11092 GAACATCCGACATGACAAACAGCGCGGCTTCTCGGTGTACACTCCGACAGAACTGCG 11151
QY 1021 GTGCTGTATGCCCTTACAGAGTAAGAACACGAGACGCGCTTGTTCACAGCAAGAGAGAA 1080
Db 11152 GTGCTGTATGCCCTTACAGAGTAAGAACACGAGACGCGCTTGTTCACAGCAAGAGAGAA 11211
QY 1081 CTCAGAGAGCTGCTGATGCTGAGGCAAGCGAGCAACGCGCGAGGCTGCTCCAG 1140
Db 11212 CTCAGAGAGCTGCTGATGCTGAGGCAAGCGAGCAACGCGCGAGGCTGCTCCAG 11271
QY 1141 CGCCATGACTGGAGAGGAGTGGGCTCTTCCCAATGCAAGAGAGAGATGATAG 1200
Db 11272 CGCCATGACTGGAGAGGAGTGGGCTCTTCCCAATGCAAGAGAGAGATGATAG 11331
QY 1201 GTAGCTGTGTGATGACGCTCCGAAAGAAATGAGACGCGCTGAGTGTGTTGCTGCA 1260
Db 11332 GTAGCTGTGTGATGACGCTCCGAAAGAAATGAGACGCGCTGAGTGTGTTGCTGCA 11391
QY 1261 CTGAACCTCTCTCTATCTTGCACATTCGCGGTTGTTTGTACATTAATAATTG 1320
Db 11392 CTGAACCTCTCTCTATCTTGCACATTCGCGGTTGTTTGTACATTAATAATTG 11451
QY 1321 CCGCGTGGCTGCAAGTGAATAATCC 1344
Db 11452 CCGCGTGGCTGCAAGTGAATAATCC 11475

RESULT 3
AX756279 1119 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 1018 from Patent WO03000905.
ACCESSION AX756279
VERSION AX756279.1 GI:32168410
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticaceae; Triticum.
REFERENCE
1 Zhu, T., Cheng, W., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T.,
Glazebrook, J., Katagiri, F., Kreps, J., Provart, N. and Riecke, D.
Identification and characterization of plant genes
Patent: WO 03000905-A 1018 03-JAN-2003;

SYNGENTA PARTICIPATIONS AG (CH)
Location/Qualifiers
1. .1119
/organism="Triticum aestivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"

ORIGIN

Query Match 27.5%; Score 370; DB 6; Length 1119;
Best Local Similarity 100.0%; Pred. No. 2.9e-93;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 961 GAACATCCGATACACACAGCGCGCTCTTCTCGGATGACCTCCGAGACAATCGC 1020
DB 727 GAACATCCGATACACACAGCGCGCTCTTCTCGGATGACCTCCGAGACAATCGC 786
QY 1021 GTCGTATGCTCCCTTACAGAGTAAGACACAGCGGCTTTTCAAGGCAAGAGAGAA 1080
DB 787 GTCGTATGCTCCCTTACAGAGTAAGACACAGCGGCTTTTCAAGGCAAGAGAGAA 846
QY 1081 CTCACAGAGCTCGTGATGTCAGCGAAGCGGCGGCGGCGGCTGCTCCAG 1140
DB 847 CTCACAGAGCTCGTGATGTCAGCGAAGCGGCGGCGGCGGCTGCTCCAG 906
QY 1141 CGGCATGACCTGGAGGGGATCGTCTCTTCCAGATGCGAGAGAGAGATGATAG 1200
DB 907 CGGCATGACCTGGAGGGGATCGTCTCTTCCAGATGCGAGAGAGAGATGATAG 966
QY 1201 GTAGCTTGTGTAGCGCTCGAAGAAATGACGCGGCTGGTGTGTGTGCTGCA 1260
DB 967 GTAGCTTGTGTAGCGCTCGAAGAAATGACGCGGCTGGTGTGTGTGCTGCA 1026
QY 1261 CTGAACCTCTCTCTATCTTGCACATTCGCCGTTGTTTGTATACATAAATAATG 1320
DB 1027 CTGAACCTCTCTCTATCTTGCACATTCGCCGTTGTTTGTATACATAAATAATG 1086
QY 1321 CCGGTGGCT 1330
DB 1087 CCGGTGGCT 1096

RESULT 4
AR340173 2853 bp DNA linear PAT 17-AUG-2003
LOCUS AR340173
DEFINITION Sequence 3 from patent US 6570066.
ACCESSION AR340173
VERSION AR340173.1 GI:33731570
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2853)
AUTHORS Willmitzer, L., Krieger, C., Luticke, S. and Lorz, H.
TITLE Nucleotide sequences encoding enzymes that alter the carbohydrate concentration and composition in plants
JOURNAL Patent: US 6570066-A 3 27-MAY-2003;
FEATURES
Location/Qualifiers
1. .2853
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 27.5%; Score 370; DB 6; Length 2853;
Best Local Similarity 100.0%; Pred. No. 3.3e-93;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 961 GAACATCCGATACACACAGCGCGCTCTTCTCGGATGACCTCCGAGACAATCGC 1020
DB 727 GAACATCCGATACACACAGCGCGCTCTTCTCGGATGACCTCCGAGACAATCGC 786
QY 1021 GTCGTATGCTCCCTTACAGAGTAAGACACAGCGGCTTTTCAAGGCAAGAGAGAA 1080
DB 787 GTCGTATGCTCCCTTACAGAGTAAGACACAGCGGCTTTTCAAGGCAAGAGAGAA 846
QY 1081 CTCACAGAGCTCGTGATGTCAGCGAAGCGGCGGCGGCGGCTGCTCCAG 1140
DB 847 CTCACAGAGCTCGTGATGTCAGCGAAGCGGCGGCGGCGGCTGCTCCAG 906
QY 1141 CGGCATGACCTGGAGGGGATCGTCTCTTCCAGATGCGAGAGAGAGATGATAG 1200
DB 907 CGGCATGACCTGGAGGGGATCGTCTCTTCCAGATGCGAGAGAGAGATGATAG 966
QY 1201 GTAGCTTGTGTAGCGCTCGAAGAAATGACGCGGCTGGTGTGTGTGCTGCA 1260
DB 967 GTAGCTTGTGTAGCGCTCGAAGAAATGACGCGGCTGGTGTGTGTGCTGCA 1026
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DB 1027 CTGAACCTCTCTCTATCTTGCACATTCGCCGTTGTTTGTATACATAAATAATG 1086
QY 1321 CCGGTGGCT 1330
DB 1087 CCGGTGGCT 1096

CTCCAGAGAGCTCGTGATGTCAGCGAAGCGGCGGCAACGCGCGGAGCTGCTCCAG 1140
DB 2539 CTCCAGAGAGCTCGTGATGTCAGCGAAGCGGCGGCAACGCGCGGAGCTGCTCCAG 2598
QY 1141 CGGCATGACCTGGAGGGGATCGTCTCTTCCAGATGCGAGAGAGAGATGATAG 1200
DB 2539 CGGCATGACCTGGAGGGGATCGTCTCTTCCAGATGCGAGAGAGAGATGATAG 2658
QY 1201 GTAGCTTGTGTAGCGCTCGAAGAAATGACGCGGCTGGTGTGTGTGCTGCA 1260
DB 2659 GTAGCTTGTGTAGCGCTCGAAGAAATGACGCGGCTGGTGTGTGTGCTGCA 2718
QY 1261 CTGAACCTCTCTCTATCTTGCACATTCGCCGTTGTTTGTATACATAAATAATG 1320
DB 2719 CTGAACCTCTCTCTATCTTGCACATTCGCCGTTGTTTGTATACATAAATAATG 2778
QY 1321 CCGGTGGCT 1330
DB 2779 CCGGTGGCT 2788

RESULT 5
TAU66376 2853 bp mRNA linear PLN 18-OCT-1996
LOCUS TAU66376
DEFINITION Triticum aestivum 1,4-alpha-D-glucan
6-alpha-D-(1,4-alpha-D-glucanotransferase mRNA, complete cds.
U66376
U66376.1 GI:1620661
ACCESSION U66376
KEYWORDS
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 2853)
AUTHORS Krieger, C., Lorz, H. and Luticke, S.
TITLE Direct Submision
JOURNAL Submitted (08-AUG-1996) University of Hamburg, Institute of General Botany, Centre of Applied Molecular Biology, AMP II, Ohnhorststr. 18, Hamburg 22609, Germany
Location/Qualifiers
1. .2853
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="T.A. Florida"
/db_xref="taxon:4565"
/feature_type="kernels 21 DAP"
313. .2502
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/note="branching enzyme"
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6-alpha-D-(1,4-alpha-D-glucanotransferase"
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ORIGIN

Query Match 27.5%; Score 370; DB 8; Length 2853;
Best Local Similarity 100.0%; Pred. No. 3.3e-93;

PUBMED 11244112
2 (bases 1 to 2726)
REFERENCE Rahman,S., Regina,A., Li,Z., Abrahams,S. and Morell,M.K.
AUTHORS Direct Submission
TITLE Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Ross,
JOURNAL Canberra, ACT 2601, Australia
location/Qualifiers
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124..2430
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NFRDEVPRIKRGYNAVOIMAOEHSYYSRGYHTNPPASRSRGTPEPDISLIR
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STPRIDRGTAHMTIRLVMGLGEGYINMGNEFGHPREMIIDPRGPOTLPTGKVLBG
NNNSYDKCRPRPLGADPLRYGMQEPDQAMHLEKYGPMTSSEHOYVRKHEEDY
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CDS
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124..2430
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KFSVAPGEIPFNIGIYDDPEEEKYVFOHPQRPESLRIRYESHIGMSPEPKINSYA
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STPRIDRGTAHMTIRLVMGLGEGYINMGNEFGHPREMIIDPRGPOTLPTGKVLBG
NNNSYDKCRPRPLGADPLRYGMQEPDQAMHLEKYGPMTSSEHOYVRKHEEDY
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LTHPHNRRSFVYTPERTAVVAVALE"

ORIGIN
Query Match 26.8%; Score 360.6; DB 8; Length 2726;
Best Local Similarity 98.4%; Pred. No. 1.5e-90;
Matches 375; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 961 GAACATCCGCATGACAAACAGCGCGCTCTTTCTCGGTGACACTCCGACAGAACTGCG 1020
DB 2347 GAACATCCGCATGACAAACAGCGCGCTCTTTCTCGGTGACACTCCGACAGAACTGCG 2406
QY 1021 GTCTGTATGCTCTTACAGAGTAAGAACCGACGCGCTGTTTCAAGGCGAAAGAGAA 1080
DB 2407 GTCTGTATGCTCTTACAGAGTAAGAACCGACGCGCTGTTTCAAGGCGAAAGAGAA 2466
QY 1081 CTCACAGAGCTGCTGATGCTGAGCGAAGCGAAGCGGCGAAGCGGCGTCTCCAAAG 1140
DB 2467 CTCACAGAGCTGCTGATGCTGAGCGAAGCGAAGCGGCGAAGCGGCGTCTCCAAAG 2526
QY 1141 CGGCATGACTGAGAGGGGATGCTGCTCTTCCACAGATGCCAGAGAGAGCATGATAG 1200
DB 2527 CGGCATGACTGAGAGGGGATGCTGCTCTTCCACAGATGCCAGAGAGAGCATGATAG 2586
QY 1201 GTAGCTTTGTTGTAGCGCTCGAAAAGAAATGACGCGGCTGGTGTGTTGTGCTGCA 1260
DB 2587 GTAGCTTTGTTGTAGCGCTCGAAAAGAAATGACGCGGCTGGTGTGTTGTGCTGCA 2646
QY 1261 CTGAACCTCTCTCTTACATCTGACATCCGCGGTGTTTGTACATATATATATTTG 1320
DB 2647 CT-AACCTCTCTCTTACATCTGACATCCGCGGTGTTTGTACATATATATTTG 2704
QY 1321 CCCGTGGCTCAACGTGAAA 1341
DB 2705 CCCGTGGCTCAACGTGAAA 2725

RESULT 8
TASBA2 2970 bp mRNA linear PLN 27-FEB-1997
LOCUS T.aestivum mRNA for starch branching enzyme II.
DEFINITION y11282.1 GI:1885343
ACCESSION y11282
VERSION 1.4-alpha-glucan branching enzyme; sbe2 gene; starch branching
KEYWORDS

SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poaceae; Triticeae; Triticum.
REFERENCE
AUTHORS Nair,R.B., Baga,M., Scoles,G.J., Karcha,K.K. and Chibbar,R.N.
TITLE Isolation, characterization and expression analysis of a starch
branching enzyme II cDNA from wheat
JOURNAL
AUTHORS Chibbar,R.N.
TITLE Direct Submission
JOURNAL 2 (bases 1 to 2970)
AUTHORS Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology
Institute, National Research Council of Canada, 110 Gymnasium
Place, Saskatoon, Saskatchewan S7N 0W9, CANADA
location/Qualifiers
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/clone="pRN33"
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1..2970
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151..2622
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QY 961 GAACATCCGCATGACAAACAGCGCGCTCTTTCTCGGTGACACTCCGACAGAACTGCG 1020
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DB 2407 GTCTGTATGCTCTTACAGAGTAAGAACCGACGCGCTGTTTCAAGGCGAAAGAGAA 2466
QY 1081 CTCACAGAGCTGCTGATGCTGAGCGAAGCGAAGCGGCGAAGCGGCGTCTCCAAAG 1140
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QY 1141 CGGCATGACTGAGAGGGGATGCTGCTCTTCCACAGATGCCAGAGAGAGCATGATAG 1200
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QY 1321 CCCGTGGCTCAACGTGAAA 1341
DB 2705 CCCGTGGCTCAACGTGAAA 2725
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polyA_signal
polyA_signal
polyA_site
polyA_site

ORIGIN
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Best Local Similarity 98.2%; Pred. No. 2.2e-90;
Matches 375; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 263 GTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGAGATAGATGATCAT 322
Db 2198 GTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGAGATAGATGATCAT 2257
QY 323 CCTCAAAAGAGAGATTTGGTATTTGTTTCAACTTCAGCTGAGCAATAGCTTTTGA 382
Db 2258 CTTGCAAAAGAGAGATTTGGTATTTGTTTCAACTTCAGCTGAGCAATAGCTTTTGA 2317
QY 383 CTAACCTGTTGGTGTTCACAGCTGGAGATGACATGCTGCTTTTCACTTTGCTCC 442
Db 2318 CTAACCTGTTGGTGTTCACAGCTGGAGATGACATGCTGCTTTTCACTTTGCTCC 2377
QY 443 ACCCTT 448
Db 2378 ACTCTT 2383
RESULT 11 1292 bp DNA linear PLN 20-APR-2003
AY235404
LOCUS Zea mays subsp. mays cultivar CML333 amylose extender starch-branching enzyme (ael) gene, exons 19 through 22 and partial cds.
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE Zea mays subsp. mays (maize)
ORGANISM Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1292)
AUTHORS Whitte,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
TITLE Genetic diversity and selection in the maize starch pathway
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
MEDLINE 22247734
PUBMED 12244216
REFERENCE 2 (bases 1 to 1292)
AUTHORS Whitte,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
TITLE Direct Submision
JOURNAL Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
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Query Match 9.9%; Score 132.4; DB 8; Length 1292;
Best Local Similarity 83.0%; Pred. No. 6.3e-26;
Matches 151; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 253 TGTAACTGCACTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGAGATAGATGATCAT 312
Db 340 TGTAACTGCACTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGAGATAGATGATCAT 399
QY 313 AGTGATCATCTCCTCAAAAGAGAGATTTGGTATTTGTTTCAACTTCAGCTGAGCAATA 372
Db 400 AGTGATCTGTGTTCGAAAGAGAGATTTGGTATTTGTTTCAACTTCAGCTGAGCAATA 459
QY 373 GCTTTTGTACTACCGTGTGGGTGTTCACAGCTGGAGATGACATGCTTGCCTT 432
Db 460 GCTATTTGTACTACCGTATTTGGTGTTCGAAAGCTGGGTGTATAGATGATCATCATC 519
QY 433 TT 434
Db 520 TT 521
RESULT 12 1373 bp DNA linear PLN 20-APR-2003
AY235395
LOCUS Zea mays subsp. mays cultivar A6 amylose extender starch-branching enzyme (ael) gene, exons 19 through 22 and partial cds.
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE Zea mays subsp. mays (maize)
ORGANISM Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1373)
AUTHORS Whitte,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
TITLE Genetic diversity and selection in the maize starch pathway
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
MEDLINE 22247734
PUBMED 12244216
REFERENCE 2 (bases 1 to 1373)
AUTHORS Whitte,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
TITLE Direct Submision
JOURNAL Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
FEATURES
source location/Qualifiers
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Best Local Similarity 83.0%; Pred. No. 6,3e-26;
Matches 151; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Db 253 TGTAACTGACGATTATGACATCTGAGCACACAGTATGTTCAAGAAACATGAGAGATA 312
390 TGTAACTGACGATTATGACATCTGATCACAGTATTTCCGAAACATGAGAGATA 449
Qy 313 AGGTATCTCTCTCAAAAGAGAGATTGGTATTTGTTTCACTTCCACTGAGAGATA 372
450 AGGTATCTCTCTCAAAAGAGAGATTGGTATTTGTTTCACTTCCACTGAGAGATA 509
Db 373 GCTTTTGGACTACCGTGTGGTGTTCAGAGCTGGAGAGTCAAGTATGCTTGCCT 432
510 GCTATTTGACTACCGTATTTGGTGTTCAGAGCTGGAGTGTAAAGTATGATCTATC 569
Qy 433 TT 434
Db 570 TT 571

RESULT 13
LOCUS AY235421 1374 bp DNA linear PLN 20-APR-2003
DEFINITION Zea mays subsp. mays cultivar TX601 amylose extender starch-branching enzyme (ae1) gene, exons 19 through 22 and partial cds.
ACCESSION AY235421 GI:30026586
VERSION AY235421.1
KEYWORDS Zea mays subsp. mays (maize)
SOURCE Zea mays subsp. mays (maize)
ORGANISM Zea mays subsp. mays (maize)
REFERENCE 1 Whitte S.R., Wilson L.M., Tenailon M.I., Gaut B.S. and Buckler E.S. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
AUTHORS Whitte S.R., Wilson L.M., Tenailon M.I., Gaut B.S. and Buckler E.S.

REFERENCE 2 (bases 1 to 1374)
TITLE Direct Submission
JOURNAL Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
MEDLINE 22447734
PUBMED 12244216
AUTHORS Whitte S.R., Wilson L.M., Tenailon M.I., Gaut B.S. and Buckler E.S.

FEATURES

SOURCE

TITLE

JOURNAL

gene

mRNA

CDS

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ORIGIN

Query Match 9.9%; Score 132.4; DB 8; Length 1374;
Best Local Similarity 83.0%; Pred. No. 6,3e-26;
Matches 151; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 253 TGTAACTGACGATTATGACATCTGAGCACACAGTATGTTCAAGAAACATGAGAGATA 312
Db 391 TGTAACTGACGATTATGACATCTGATCACAGTATTTCCGAAACATGAGAGATA 450
Qy 313 AGGTATCTCTCTCAAAAGAGAGATTGGTATTTGTTTCACTTCCACTGAGAGATA 372
Db 451 AGGTATCTCTCTCAAAAGAGAGATTGGTATTTGTTTCACTTCCACTGAGAGATA 510
Qy 373 GCTTTTGGACTACCGTGTGGTGTTCAGAGCTGGAGAGTCAAGTATGCTTGCCT 432
Db 511 GCTATTTGACTACCGTATTTGGTGTTCAGAGCTGGAGTGTAAAGTATGATCTATC 570
Qy 433 TT 434
Db 571 TT 572

RESULT 14
LOCUS AY235405 1382 bp DNA linear PLN 20-APR-2003
DEFINITION Zea mays subsp. mays cultivar D940Y amylose extender starch-branching enzyme (ae1) gene, exons 19 through 22 and partial cds.
ACCESSION AY235405
VERSION AY235405.1
KEYWORDS Zea mays subsp. mays (maize)
SOURCE Zea mays subsp. mays (maize)
ORGANISM Zea mays subsp. mays (maize)
REFERENCE 1 Whitte S.R., Wilson L.M., Tenailon M.I., Gaut B.S. and Buckler E.S. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
AUTHORS Whitte S.R., Wilson L.M., Tenailon M.I., Gaut B.S. and Buckler E.S.

REFERENCE 2 (bases 1 to 1382)
TITLE Direct Submission
JOURNAL Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
MEDLINE 22447734
PUBMED 12244216
AUTHORS Whitte S.R., Wilson L.M., Tenailon M.I., Gaut B.S. and Buckler E.S.

FEATURES

SOURCE

TITLE

JOURNAL

gene

mRNA

CDS

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 01:51:55 ; Search time 525.86 Seconds
(without alignments)
10857.595 Million cell updates/sec

Title: US-09-508-377-10_COPY_10120_11463

Perfect score: 1344
Sequence: 1 ttgataatcgtggtatgcacaa.....tgcctcaacgtgaataacc 1344

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1344	100.0	11473	2	AAAX34650 Starch br
2	1344	100.0	11475	5	AAH78338 Nucleotid
3	370	27.5	1119	9	ADCO8713 Wheat DNA
4	367.4	27.3	979	3	AAZ99942 Nucleotid
5	360.6	26.8	2726	3	AAH78337 Nucleotid
6	360	26.8	984	3	AAZ99946 Nucleotid
7	347.6	25.9	977	3	AAZ99947 Nucleotid
8	146	10.9	1085	3	AAZ99962 Consensus
9	132.4	9.9	23449	3	AAZ53393 Maize amy
10	125.6	9.3	2307	3	AAZ99938 DNA encod
11	124.4	9.3	2307	3	ADCO7807 Rice DNA
12	124.2	9.2	1120	3	AAZ99941 Nucleotid
13	124	9.2	1087	3	AAZ99940 Nucleotid
14	123.4	9.2	2304	9	ADCO8218 Rice DNA
15	123.4	9.2	2555	7	ADCO8218 Rice DNA
16	123.4	9.2	3015	7	AAV05639 Rice gene
17	122.6	9.1	1036	3	AAZ99939 Nucleotid
18	122.6	9.1	2968	5	AAH78342 Nucleotid
19	122.6	9.1	3039	6	AAH78342 Nucleotid
20	122.4	9.1	1267	9	ADCO8721 Wheat sta
21	120.6	9.0	636	9	ADCO8852 Corn DNA
22	120.6	9.0	2640	2	AAV70961 DNA encod
23	120.6	9.0	2665	2	AAH69729 Plasmid p

24	120.6	9.0	2725	2	AAV29757 Zea mays
25	112.4	8.4	2919	2	AAQ73750 Rice star
26	106.2	7.9	2283	9	ADCO7805 Rice DNA
27	97	7.2	602	6	ABQ66378 Arabidops
28	97	7.2	2418	6	ABZ13067 Arabidops
29	97	7.2	2418	7	ADA68438 Arabidops
30	95.4	7.1	2529	2	AAH42637 Class A s
31	95.4	7.1	2531	2	AAH42637 Class A s
32	92.6	6.9	2975	2	AAH42635 Class A s
33	91.4	6.8	1919	2	AAV38722 CDNA enc
34	91.4	6.8	3090	2	AAV38720 Potato BE
35	91	6.8	1255	7	AAZ51329 Potato BE
36	91	6.8	2563	5	ABK50301 Potato CD
37	91	6.8	2576	2	AAH42636 Class A s
38	91	6.8	2578	2	AAH42631 Class A s
39	91	6.8	3074	2	AAH69587 Potato st
40	89.4	6.7	3231	2	AAH42632 Class A s
41	89.4	6.7	1069	2	AAV38721 CDNA enc
42	89.4	6.7	2913	2	AAV38719 Full leng
43	89.4	6.7	3003	2	AAH42634 Class A s
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ALIGNMENTS

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AAX34650 standard; DNA; 11473 BP.
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XX AAX34650;
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XX 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
XX
XX Starch branching enzyme II (SBE II) gene sequence.
DE
XX Starch biosynthetic pathway; cereal plant; enzyme; SBE, SSS, DBE, GBSG;
KW starch branching enzyme; starch soluble synthase; debranching enzyme;
KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;
KW grain softness protein I; bacterial isoamylase; glycogen synthase;
KM WSBF 1-D4 gene; ss.
XX
XX Aegilops tauschii.
OS
XX
XX WO9914314-A1.
PN
XX
XX 25-MAR-1999.
PD
XX
XX 11-SEP-1998; 98WO-AU000743.
PF
XX 12-SEP-1997; 97AU-00009108.
PR 20-MAR-1998; 98AU-00002509.
PR
XX
XX (CSTR) COMMONWEALTH SCI & IND RES ORG.
PA (AUSU) UNIV AUSTRALIAN NAT.
PA (GOOD-) GOODMAN FIELDER LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
PA
XX
XX Li Z, Morell M, Rahman S;
PI
XX
XX WPI; 1999-229525/19.
DR
XX
XX New isolated cereal plant enzyme genes used for, e.g. expression of
PT antisense sequences of granule bound synthase.
PT
XX
XX Claim 8; Page 75-81; 171pp; English.
PS
XX
XX The invention relates to a novel enzyme of starch biosynthetic pathway in
CC a cereal plant, where the enzyme is selected from starch branching enzyme
CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme
CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of

CC rice or maize. The methods and products can be used for targeting
 CC expression specifically to the endosperm of the seeds of cereal plants
 CC such as wheat or barley. They can be used for the expression of e.g.
 CC antisense sequences of granule-bound synthase (GBS), SBE II, low mol.
 CC wt. glutenin, grain softness protein 1, bacterial isomylase, bacterial
 CC glycogen synthase, and wheat high mol. wt. glutenin Bx1. They can be
 CC used for modifying the characteristics of starch produced by a plant. The
 CC present sequence represents the SBE II gene sequence. (Updated on 17-OCT-
 CC 2003 to standardise OS field)
 CC XX
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 Query Match 100.0%; Score 1344; DB 2; Length 11473;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTAGATATCGTGTATGCAAGAGTTCGATCAGCAGCATGCGATCTTGAAGAAAATATG 60
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 QY 61 GGGATATGCTAGTGGTTTGTCTTTGTTCATTAACAAGTCAAGTTAAGCTCTCTTC 120
 DB 10190 GGGATATGCTAGTGGTTTGTCTTTGTTCATTAACAAGTCAAGTTAAGCTCTCTTC 10249
 QY 121 AAGTGTATTAAGTGTATTAATTAATTCCTATAGATGAAAACCTGCAAGGCGG 180
 DB 10250 AAGTGTATTAAGTGTATTAATTAATTCCTATAGATGAAAACCTGCAAGGCGG 10309
 QY 181 AGCTGAATGCTTTTCAACCAAACTATTTTCTTAAGTCTGTGATGATACATATAC 240
 DB 10310 AGCTGAATGCTTTTCAACCAAACTATTTTCTTAAGTCTGTGATGATACATATAC 10369
 QY 241 CAGCACTGACATGTACTGACAGTTTATGACATCTGACACAGTATGTTTCAACGGAAC 300
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 QY 361 ACTGAGAGCAATAGCTTTTGTGACTACCGTGGGAGTTCACAGCCTGGGAAAGTACAAG 420
 DB 10490 ACTGAGAGCAATAGCTTTTGTGACTACCGTGGGAGTTCACAGCCTGGGAAAGTACAAG 10549
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 DB 10550 TATGCTTCCCTTTTCAATGTCACCCCTTCACAGTATGAGGTTATGAGGAGCTTCTACACT 10609
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 DB 10730 CCCCAGACACATACCATTCATTCATATATATCTAATTAAGTGTGTTTCAATCTTATG 10789
 QY 661 CTCAGTTGAGCTCGGTCTAATCTAGAACTATTTTCCGAATCAACCTAACCTCTACG 720
 DB 10790 CTCAGTTGAGCTCGGTCTAATCTAGAACTATTTTCCGAATCAACCTAACCTCTACG 10849
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 QY 781 GCTATTTCTTAATCAGTGGCTTGTGACTCTGACATGACATCTCTTGTGATTCAGCAG 840
 DB 10910 GCTATTTCTTAATCAGTGGCTTGTGACTCTGACATGACATCTCTTGTGATTCAGCAG 10969
 QY 841 GCTTATATATATGTCATCTTCAACACGTAAGTCTGAGGCTCAAGGCTACCTGACT 900

DB 10970 GCTTATATATATGTCATCTTCAACACGTAAGTCTGAGGCTCAAGGCTACCTGACT 11029
 QY 901 CGTCTTGAATCAATGCTTCAAAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 960
 DB 11030 CGTCTTGAATCAATGCTTCAAAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 11089
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 QY 1021 GTGCTGATGCTCTTCAAGTAAAGAACAGCAGCAGCTTGTACAAAGCAAAAGAGAGA 1080
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 QY 1141 CGCATGACTGGAGAGGAGATCGTCTCTTCCCAATGCTCAAGAGAGAGAGATGATGATG 1200
 DB 11270 CGCATGACTGGAGAGGAGATCGTCTCTTCCCAATGCTCAAGAGAGAGAGATGATGATG 11329
 QY 1201 GTAGCTTGTGTGAGAGGCTCGAAAGAAATGACAGGAGCTGGGTTGTTGTGCTGCA 1260
 DB 11330 GTAGCTTGTGTGAGAGGCTCGAAAGAAATGACAGGAGCTGGGTTGTTGTGCTGCA 11389
 QY 1261 CTGAACCTCTCTCTATCTTGAACATTCGCGTGTGTTTGTATCAATATATATATG 1320
 DB 11390 CTGAACCTCTCTCTATCTTGAACATTCGCGTGTGTTTGTATCAATATATATATG 11449
 QY 1321 CCGTGGCTGCAACGTGAATAATCC 1344
 DB 11450 CCGTGGCTGCAACGTGAATAATCC 11473

RESULT 2
 AAH78338
 ID AAH78338 standard, cDNA, 11475 BP.
 XX
 AC AAH78338;
 XX
 DT 26-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of a starch branching enzyme designated F2.
 XX
 KW Wheat; starch branching enzyme; BE1b; SBE; transgenic plant;
 XX search biosynthetic pathway; amylopectin; F2; amylose; ss.
 XX
 OS Aegilops tauschii.
 XX
 PN WO200162934-A1.
 XX
 PD 30-AUG-2001.
 XX
 PF 21-FEB-2001; 2001MO-AU000175.
 XX
 PR 21-FEB-2000; 2000AU-00005742.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX (GOOD-) GOODMAN FIELDER LTD.
 XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
 XX
 PI Morell M, Rahman S;
 XX
 DR WPI; 2001-570635/64.
 XX
 PT Nucleic acids encoding wheat starch branching enzyme IIb, useful for
 XX altering the amylose and amylopectin content of cereal plants, e.g. wheat
 XX and barley.
 PS Example 1; Fig 2; 103pp; English.
 XX

PT nutritional properties.
XX
XX Disclosure; SEQ ID NO 1018; 130pp; English.
XX
XX This invention, in the area of plant biotechnology, relates to novel
CC polynucleotides comprising a nucleotide sequence encoding a protein which
CC is involved in or associated with the synthesis, metabolism or
CC degradation of carbohydrates in the plant grain and the expression of
CC which is up-regulated during grain filling. The plant is selected from
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
CC sugarbeet, wheat, and rice. The invention may be useful for the
CC improvement of protein, oil, starch, fibre and moisture content of the
CC cereal grains. In addition, carbohydrate levels may be modified to a more
CC desirable level using the present invention. The present sequence is a
CC DNA sequence from wheat which showed homology to rice "grain filling"
CC genes of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences.
XX
SQ Sequence 1119 BP; 295 A; 234 C; 291 G; 299 T; 0 U; 0 Other;

Query Match 27.5%; Score 370; DB 9; Length 1119;
Best Local Similarity 100.0%; Pred. No. 9,4e-106; Indels 0; Gaps 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 961 GAACATCCGCATGACACAGAGCGCGCTCTTCTCGGTATCACTCCGAGAGAACTGCG 1020
DB 727 GAACATCCGCATGACACAGAGCGCGCTCTTCTCGGTATCACTCCGAGAGAACTGCG 786
OY 1021 GTCTGTATGCTCTTACAGATGAAGAACAGAGCGCTTGTATCAAGCAAGAGAGAA 1080
DB 787 GTCTGTATGCTCTTACAGATGAAGAACAGAGCGCTTGTATCAAGCAAGAGAGAA 846
OY 1081 CTCACAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
DB 847 CTCACAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 906
OY 1141 CGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 907 CGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 966
OY 1201 GTAGCTTGTGTGAGCGCTCGAAGAAATGACGCGCTGTTGTGTGTGTGTGTGTGTG 1260
DB 967 GTAGCTTGTGTGAGCGCTCGAAGAAATGACGCGCTGTTGTGTGTGTGTGTGTGTG 1026
OY 1261 CTGAACCTCTCTCTATCTTGTGACATCCCGGTTGTTGTATATTAATAATTG 1320
DB 1027 CTGAACCTCTCTCTATCTTGTGACATCCCGGTTGTTGTATATTAATAATTG 1086
OY 1321 CCGGTGCGCT 1330
DB 1087 CCGGTGCGCT 1096

PF 09-SEP-1999; 99WO-GB003011.
XX
XX 10-SEP-1998; 99EP-00307337.
XX
XX (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.
XX
XX Goldsbrough A, Collier S;
XX
XX WPI; 2000-271446/23.
XX
XX DNA encoding wheat starch branching enzyme II isoforms, useful in
PT altering the characteristics of a plant, especially elevated starch
PT gelatinization onset and/or peak temperature.
XX
XX Claim 5; Page 124; 197pp; English.
XX
XX The present sequence represents a clone of wheat starch branching enzyme
CC II (SBEII), which is part of a novel subclass of known SBEII genes,
CC designated SBEII-2, subclass B (SBEII-2B). The specification also
CC describes subclasses SBEII-1 genes, which are thought to have similar
CC functional properties to the maize SBEII gene. Starch branching enzymes
CC catalyse the formation of the alpha-1,6 linkages, creating branch points
CC in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage
CC followed by reattachment of the released alpha-1,4-glucan chain to the
CC same or another glucosyl chain. SBEII polypeptides can be used to alter
CC the characteristics of a plant, in particular to alter starch so that it
CC has an elevated gelatinization onset and/or peak temperature. Starch
CC obtained from transgenic plants is useful in the preparation or
CC processing a foodstuff, particularly bakery products
XX
SQ Sequence 979 BP; 271 A; 203 C; 247 G; 257 T; 0 U; 1 Other;

Query Match 27.3%; Score 367.4; DB 3; Length 979;
Best Local Similarity 99.5%; Pred. No. 5.8e-105;
Matches 368; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 961 GAACATCCGCATGACACAGAGCGCGCTCTTCTCGGTATCACTCCGAGAGAACTGCG 1020
DB 558 GAACATCCGCATGACACAGAGCGCGCTCTTCTCGGTATCACTCCGAGAGAACTGCG 617
OY 1021 GTCTGTATGCTCTTACAGATGAAGAACAGAGCGCTTGTATCAAGCAAGAGAGAA 1080
DB 618 GTCTGTATGCTCTTACAGATGAAGAACAGAGCGCTTGTATCAAGCAAGAGAGAA 677
OY 1081 CTCACAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
DB 678 CTCACAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 737
OY 1141 CGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 738 CGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 797
OY 1201 GTAGCTTGTGTGAGCGCTCGAAGAAATGACGCGCTGTTGTGTGTGTGTGTGTGTG 1260
DB 798 GTAGCTTGTGTGAGCGCTCGAAGAAATGACGCGCTGTTGTGTGTGTGTGTGTGTG 857
OY 1261 CTGAACCTCTCTCTATCTTGTGACATCCCGGTTGTTGTATATTAATAATTG 1320
DB 858 CTGAACCTCTCTCTATCTTGTGACATCCCGGTTGTTGTATATTAATAATTG 917
OY 1321 CCGGTGCGCT 1330
DB 918 CCGGTGCGCT 927

RESULT 4
AAZ99942
ID AAZ99942 standard; DNA; 979 BP.
XX
XX AAZ99942;
XX
XX 25-JUL-2000 (first entry)
XX
XX Nucleotide sequence of starch branching enzyme II clone B1.
XX
XX wheat; starch branching enzyme II; SBEII; SBEII-2; starch; SBEII-1;
XX gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.
XX
XX Triticum aestivum.
XX
XX MO200015810-A1.
XX
XX 23-MAR-2000.
XX

RESULT 5
AAH78337
ID AAH78337 standard; cDNA; 2726 BP.
XX
XX AAH78337;
XX
XX 26-NOV-2001 (first entry)
XX

```
DE Nucleotide sequence of wheat starch branching enzyme 9 (BEIIa).
XX Wheat; starch branching enzyme; BEIIa; BEIIb; SBE; transgenic plant;
KW starch biosynthetic pathway; amylopectin; amylose; ss.
XX
XX Triticum sp.
XX WO200162934-A1.
XX
XX 30-AUG-2001.
XX
XX 21-FEB-2001; 2001WO-AU000175.
XX
XX 21-FEB-2000; 2000AU-00005742.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PA (GOOD-) GOODMAN FIELDER LTD.
XX PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX
XX Morell M, Rahman S;
XX PI
XX DR WPI; 2001-570635/64.
XX
XX Nucleic acids encoding wheat starch branching enzyme IIb, useful for
XX PT altering the amylose and amylopectin content of cereal plants, e.g. wheat
XX PT and barley.
XX
XX Example 1; Fig 1; 103bp; English.
XX
XX The present sequence encodes wheat starch branching enzyme 9, designated
XX BEIIa. The specification describes BEIIb. BEIIb is a type II starch
XX branching enzyme (SBE). The BEIIb nucleic acids may be used to
XX genetically transform cereal plants such as wheat or barley and for
XX altering their nutritional content by modulating the starch biosynthetic
XX pathway to vary levels of amylopectin and/or amylose produced in the
XX plant.
XX
XX Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 U; 0 Other;
SQ
Query Match 26.8%; Score 360.6; DB 5; Length 2726;
Best Local Similarity 98.4%; Pred. No. 1.5e-102;
Matches 375; Conservative 0; Mismatches 4; Indels 2; Gaps 1;
OY 961 GAACATCCGCATGACAAACAGCGCGCTCTTTCTCGGTGACACTCCGAGCAAACTGCG 1020
DB 2347 GAACATCCGCATGACAAACAGCGCGCTCTTTCTCGGTGACACTCCGAGCAAACTGCG 2406
OY 1021 GTCGTGTATGCCCTTACAGAGTAAGAAACAGCGCGCTGTTACAGAGCAAGAGAGAA 1080
DB 2407 GTCGTGTATGCCCTTACAGAGTAAGAAACAGCGCGCTGTTACAGAGCAAGAGAGAA 2466
OY 1081 CTCGAGAGAGCTCGTGATCGTAGAGCAAGCGAGCAAGCGCGCGAGCTGCTCCAG 1140
DB 2467 CTCGAGAGAGCTCGTGATCGTAGAGCAAGCGAGCAAGCGCGCGAGCTGCTCCAG 2526
OY 1141 CGCCATGACTGGAGAGGAGTCTGCTCTTCCCAAGATGCCAGAGAGAGAGATGAGTAG 1200
DB 2527 CGCCATGACTGGAGAGGAGTCTGCTCTTCCCAAGATGCCAGAGAGAGAGATGAGTAG 2586
OY 1201 GTAGCTGTGTGGAGAGCGCTCGAAAGAAATGAGCGGCGCTGGGTGTTGTGTCGCGCA 1260
DB 2587 GTAGCTGTGTGGAGAGCGCTCGAAAGAAATGAGCGGCGCTGGGTGTTGTGTCGCGCA 2646
OY 1261 CTGAACCTCTCTCTTACTTGTGACATTCGCGTGTGTTTGTACATAAATAAATTG 1320
DB 2647 CT--ACCTCTCTCTTACTTGTGACATTCGCGTGTGTTTGTACATAAATAAATTG 2704
OY 1321 CCGGTGCGCTCAACGTGAAA 1341
DB 2705 CCGGTGCGCTCAACGTGAAA 2725
OY
DB

AAZ99946
ID AAZ99946 standard; DNA; 984 BP.
XX
XX AAZ99946;
XX
XX 25-JUL-2000 (first entry)
XX
XX Nucleotide sequence of starch branching enzyme II clone AZ.
XX
XX Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2;
XX KW gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.
XX
XX Triticum aestivum.
XX
XX WO200015810-A1.
XX
XX 23-MAR-2000.
XX
XX 09-SEP-1999; 99WO-GB003011.
XX
XX 10-SEP-1998; 98EP-00307337.
XX
XX (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.
XX
XX Goldsbrough A, Colliver S;
XX PI
XX DR WPI; 2000-271446/23.
XX
XX DNA encoding wheat starch branching enzyme II isoforms, useful in
XX PT altering the characteristics of a plant, especially elevated starch
XX PT gelatinization onset and/or peak temperature.
XX
XX Disclosure; Page 168; 197pp; English.
XX
XX The present sequence represents a clone of wheat starch branching enzyme
XX II (SBEII), which is part of a novel subclass of known SBEII genes,
XX designated SBEII-1. The specification also describes subclass SBEII-2
XX sequences. The SBEII-1 genes are thought to have similar functional
XX properties to the maize SBEIIb gene. Starch branching enzymes catalyse
XX the formation of the alpha-1,6 linkages, creating branch points in the
XX growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed
XX by reattachment of the released alpha-1,4-glucan chain to the same or
XX another glucosyl chain. SBEII polypeptides can be used to alter the
XX characteristics of a plant, in particular to alter starch so that it has
XX an elevated gelatinisation onset and/or peak temperature. Starch obtained
XX from transgenic plants is useful in the preparation or processing a
XX foodstuff, particularly bakery products
XX
XX Sequence 984 BP; 268 A; 212 C; 250 G; 254 T; 0 U; 0 Other;
SQ
Query Match 26.8%; Score 360; DB 3; Length 984;
Best Local Similarity 98.2%; Pred. No. 1.3e-102;
Matches 375; Conservative 0; Mismatches 5; Indels 2; Gaps 1;
OY 961 GAACATCCGCATGACAAACAGCGCGCTCTTTCTCGGTGACACTCCGAGCAAACTGCG 1020
DB 558 GAACATCCGCATGACAAACAGCGCGCTCTTTCTCGGTGACACTCCGAGCAAACTGCG 617
OY 1021 GTCGTGTATGCCCTTACAGAGTAAGAAACAGCGCGCTGTTACAGAGCAAGAGAGAA 1080
DB 618 GTCGTGTATGCCCTTACAGAGTAAGAAACAGCGCGCTGTTACAGAGCAAGAGAGAA 677
OY 1081 CTCGAGAGAGCTCGTGATCGTAGAGCAAGCGAGCAAGCGCGCGAGCTGCTCCAG 1140
DB 678 CTCGAGAGAGCTCGTGATCGTAGAGCAAGCGAGCAAGCGCGCGAGCTGCTCCAG 737
OY 1141 CGCCATGACTGGAGAGGAGTCTGCTCTTCCCAAGATGCCAGAGAGAGAGATGAGTAG 1200
DB 738 CGCCATGACTGGAGAGGAGTCTGCTCTTCCCAAGATGCCAGAGAGAGAGATGAGTAG 797
OY 1201 GTAGCTGTGTGGAGAGCGCTCGAAAGAAATGAGCGGCGCTGGGTGTTGTGTCGCGCA 1260
DB 798 GTAGCTGTGTGGAGAGCGCTCGAAAGAAATGAGCGGCGCTGGGTGTTGTGTCGCGCA 857
OY
DB
```

QY 1261 CTGAACCTCTCCCTATCTTGACATTCGCGTGTGTTTGTACATATACTAATTAATG 1320
DB 858 CT--ACCTCTCTCTATCTTGACATTCGCGTGTGTTTGTACATATACTAATTAATG 915
QY 1321 CCCGTGCGCTCAACGTGAAAT 1342
DB 916 CCGGTGCGCTCAACGTGAAAT 937
RESULT 7
AAZ99947
ID AAZ99947 standard; DNA; 977 BP.
AC AAZ99947;
XX
XX 25-JUL-2000 (first entry)
DE Nucleotide sequence of starch branching enzyme II clone B11.
XX
XX Wheat; starch branching enzyme II; SBEII-1; starch; SBEII-2; starch; SBEII-2;
KM gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.
XX
XX Triticum aestivum.
OS
FH Key Location/Qualifiers
FT CDS 3..641
FT /*tag= a
FT /product= "starch branching enzyme II"
XX
XX WO200015810-A1.
XX
XX 23-MAR-2000.
PD
PF 09-SEP-1999; 99WO-GB003011.
XX
XX 10-SEP-1998; 98EP-00307337.
PR
PA (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.
XX
PI Goldbrough A, Colliver S;
XX
XX MPI; 2000-271446/23.
DR P-PSDB; AAY64411.
XX
XX DNA encoding wheat starch branching enzyme II isoforms, useful in
PT altering the characteristics of a plant, especially elevated starch
PT gelatinization onset and/or peak temperature.
XX
PS Disclosure; Page 168-169; 197P; English.
XX
XX The present sequence represents a clone of wheat starch branching enzyme
CC II (SBEII), which is part of a novel subclass of known SBEII genes,
CC designated SBEII-1. The specification also describes subclass SBEII-2
CC sequences. The SBEII-1 genes are thought to have similar functional
CC properties to the maize SBEIIb gene. Starch branching enzymes catalyze
CC the formation of the alpha-1,6 linkages, creating branch points in the
CC growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed
CC by reattachment of the released alpha-1,4-glucan chain to the same or
CC another glucosyl chain. SBEII polypeptides can be used to alter the
CC characteristics of a plant, in particular to alter starch so that it has
CC an elevated gelatinisation onset and/or peak temperature. Starch obtained
CC from transgenic plants is useful in the preparation or processing a
CC foodstuff, particularly bakery products
XX
SQ Sequence 977 BP; 270 A; 200 C; 245 G; 262 T; 0 U; 0 Other;
Query Match 25.9%; Score 347.6; DB 3; Length 977;
Best Local Similarity 96.2%; Pred. No. 1.1e-98;
Matches 356; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 961 GAATATCCGATGACAGAGCGCGCTTCTTGCGGTACACCCGAGAGAACTGCG 1020

DB 558 GAATATCCGATGACAGAGCGCGCTTCTTGCGGTACACCTCTAGAGAACTGCG 617
QY 1021 GTCGTATGTCCTCTTACAGAGTACAGACGAGCGGCTGTTTACAGAGAAAGAGAA 1080
DB 618 GTCGTATGTCCTCTTACAGAGTACAGACGAGCGGCTGTTTACAGAGAAAGAGAA 677
QY 1081 CTCCAGAGAGCTCTGTAATCGTAGACGAGCGAGCGGCGAGGCTGCTCAAG 1140
DB 678 CTCAGAGAGCTCTGTAATCGTAGACGAGCGAGCGGCTGCTGCTTAAAG 737
QY 1141 CGCCATGACTGAGAGGAGATGCTGCTCTTCCCGAGATCCAGAGAGAGATGATAG 1200
DB 738 CGCCATGACTGAGAGGAGATGCTGCTCTTCCCGAGATCCAGAGAGAGATGATAG 797
QY 1201 GTAGCTTGTGCTGAGCGCTGGAAGAAAGAAATGAGCGGCTGCTGCTGCA 1260
DB 798 GTAGCTTGTGCTGAGCGCTGGAAGAAAGAAATGAGCGGCTGCTGCTGCA 857
QY 1261 CTGAACCTCTCCCTATCTTGACATTCGCGTGTGTTTGTACATATACTAATTAATG 1320
DB 858 CTGAACCTCTCCCTATCTTGACATTCGCGTGTGTTTGTACATATACTAATTAATG 917
QY 1321 CCGGTGCGCT 1330
DB 918 CCGGTGCGCT 927
RESULT 8
AAZ99962
ID AAZ99962 standard; DNA; 1085 BP.
AC AAZ99962;
XX
XX 25-JUL-2000 (first entry)
DE
XX
XX Consensus sequence of starch branching enzyme II.
XX
XX Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2;
KM gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.
XX
XX Triticum aestivum.
OS
FH Key Location/Qualifiers
FT CDS 3..1085
FT /*tag= a
FT /product= "starch branching enzyme II"
XX
XX WO200015810-A1.
XX
XX 23-MAR-2000.
PD
PF 09-SEP-1999; 99WO-GB003011.
XX
XX 10-SEP-1998; 98EP-00307337.
PR
PA (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.
XX
PI Goldbrough A, Colliver S;
XX
XX MPI; 2000-271446/23.
DR
XX
XX DNA encoding wheat starch branching enzyme II isoforms, useful in
PT altering the characteristics of a plant, especially elevated starch
PT gelatinization onset and/or peak temperature.
XX
PS Disclosure; Page 187; 197P; English.
XX
XX The present sequence represents the consensus sequence of wheat starch
CC branching enzyme II (SBEII). The specification describes novel subclasses
CC of SBEII, designated SBEII-1 and SBEII-2. The SBEII-1 genes are thought
CC to have similar functional properties to the maize SBEIIb gene. Starch
CC branching enzymes catalyze the formation of the alpha-1,6 linkages,
CC creating branch points in the growing starch molecule, via hydrolysis of
CC an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-
CC glucan chain to the same or another glucosyl chain. SBEII polypeptides
CC can be used to alter the characteristics of a plant, in particular to
CC alter starch so that it has an elevated gelatinisation onset and/or peak
CC temperature. Starch obtained from transgenic plants is useful in the

CC preparation or processing a foodstuff, particularly bakery products

XX Sequence 1085 BP; 268 A; 185 C; 284 G; 348 T; 0 U; 0 Other;

Query Match 10.9%; Score 146; DB 3; Length 1085;

Best Local Similarity 86.6%; Pred. No. 6.5e-35; Matches 161; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 263 GTTATGACATCTGAGACCACTATGTTTACCGAAACATGAGGAATAGATGATCAT 322

DB 326 GTTATGACATCTGAGACCACTATGTTTACCGAAACATGAGGAATAGATGATCAT 385

QY 323 CCTGAAAGAGGAGATTGGTATTTGTTTCACTTCAGAGCAATAGCTTTTGA 382

DB 386 GTTGAAGAGGAGATTGGTATTTGTTTCACTTCAGAGCAATAGCTTTTGA 445

QY 383 CTACCGTGTGGTGTTCACAGCCTGGGAGATACAGAGTATGCTTGCTTTTCATTGTCC 442

DB 446 CTACCGTGTGGTGTTCACAGCCTGGGAGATACAGAGTATGCTTGCTTGCTCGACGCTGG 505

QY 443 ACCCTT 448

DB 506 ACTCTT 511

RESULT 9

AAZ35393 ID AAZ35393 standard; DNA; 23449 BP.

XX AAZ35393;

DT 27-MAR-2000 (first entry)

DE Maize amylose-extender (Ae) gene encoding starch branching enzyme.

XX Starch branching enzyme Iib; amylose-extender gene; Ae gene; maize; corn;

KM promoter; expression control element; endospERM; transgenic plant; ss.

XX Zea mays.

XX Key Location/Qualifiers

FT 597..602 /tag= a

FT /note= "I box, conserved in RBCS genes"

FT 1475..1481 /tag= b

FT /note= "RY repeat, distal regulatory element"

FT 1967..1973 /tag= c

FT /note= "Hex, conserved element found in plant histone

FT gene promoters"

FT 2593..2599 /tag= d

FT /note= "KRE box, motif essential for metal ion-dependent

FT induction of metallothionein genes"

FT 2666..2671 /tag= e

FT /tag= f

FT 2738..2743 /tag= g

FT 2831..2836 /tag= h

FT 2838..2844 /tag= i

FT /tag= j

FT /note= "KRE box, motif essential for metal ion-dependent

FT /tag= k

FT /note= "contains introns"

FT 3177..3282 /tag= m

FT /number= 1

FT 3283..3428 /tag= n

FT /number= 2

FT 3429..3672 /tag= o

FT /number= 2

FT 3673..3827 /tag= p

FT /number= 3

FT 3828..4913 /tag= q

FT /number= 3

FT 4914..5012 /tag= r

FT /number= 4

FT 5013..5088 /tag= s

FT /number= 4

FT 5089..5131 /tag= t

FT /number= 5

FT 5132..5327 /tag= u

FT /number= 5

FT 5328..5387 /tag= v

FT /number= 6

FT 5388..5886 /tag= w

FT /number= 6

FT 5887..5967 /tag= x

FT /number= 7

FT 5968..6048 /tag= y

FT /number= 7

FT 6049..6165 /tag= z

FT /number= 8

FT 6166..6750 /tag= aa

FT /number= 8

FT 6751..6816 /tag= ab

FT /number= 9

FT 6817..7591 /tag= ac

FT /number= 9

FT 7592..7713 /tag= ad

FT /number= 10

FT 7714..8464 /tag= ae

FT /number= 10

FT 8465..8584 /tag= af

FT /number= 11

FT 8585..12604 /tag= ag

FT /number= 11

FT 12605..12734 /tag= ah

FT /number= 12

FT 12735..12820 /tag= ai

FT /number= 12

FT 12821..12931 /tag= aj

FT /number= 12

FT			/number= 13
FT	intron		12937..13079
PT		/*tag= ak	
FT		/number= 13	
FT	exon		13080..13208
FT		/*tag= al	
FT		/number= 14	
FT	intron		13209..16259
FT		/*tag= am	
FT		/number= 14	
PT	exon		16260..16363
PT		/*tag= an	
PT		/number= 15	
FT	intron		16364..17255
PT		/*tag= ao	
PT		/number= 15	
PT	exon		17236..17380
PT		/*tag= ap	
PT		/number= 16	
FT	intron		17381..17837
FT		/*tag= aq	
FT		/number= 16	
FT	exon		17838..17985
FT		/*tag= ar	
FT		/number= 17	
FT	intron		17986..18129
FT		/*tag= as	
FT		/number= 17	
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FT		/*tag= at	
FT		/number= 18	
FT	intron		18231..18458
PT		/*tag= au	
PT		/number= 18	
PT	exon		18457..18534
PT		/*tag= av	
PT		/number= 19	
FT	intron		18535..18800
FT		/*tag= aw	
FT		/number= 19	
FT	exon		18801..18956
FT		/*tag= ax	
FT		/number= 20	
FT	intron		18957..19404
FT		/*tag= ay	
FT		/number= 20	
FT	exon		19405..19479
FT		/*tag= az	
FT		/number= 21	
FT	intron		19480..19575
FT		/*tag= ba	
FT		/number= 21	
FT	exon		19576..19659
FT		/*tag= bb	
FT		/number= 22	
FT	polya_signal		19643..19849
FT		/*tag= bc	
FT	misc_feature		23089..23101
FT		/*tag= bd	
XX			
PN	W09964562-A2.		
PD	16-DEC-1999.		
XX			
PB	11-JUN-1999;	99WC-U08013266.	
XX			
PR	12-JUN-1998;	98US-U089049P.	
XX	12-JUN-1998;	98US-U089050P.	
PA	(UPE-) UNIV PENNSYLVANIA STATE		
XX			
PL	Gultinan MJ, Kim K;		
XX			

DR	WPI; 2000-116538/10.
XX	
PT	New gene regulatory sequences from plants used to provide resistance to
PT	microbial path pathogens.
XX	
PS	Claim 19; Page 98-105; 110pp; English.
XX	
CC	This is the nucleotide sequence of the maize amylose-extender (Ae) gene
	Query Match 9.9%; Score 132.4; DB 3; Length 23449;
	Best Local Similarity 83.0%; Pred. No. 8.3e-30;
	Matches 151; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY	253 TGTAACTGAGTTTATGACATCTGACACACAGATGTTTTCACGGAACATGAGAGAATA 312
DB	18790 TGTAACTGAGTTTATGACATCTGACACACAGATGTTTTCACGGAACATGAGAGAATA 18849
QY	313 AGGTATCATCTCTCAAAAGAGAGATTTGGTATTTGTTTCACTTCATGAGCAATA 372
DB	18850 AGGTATCTGTGTTGCAAAAAGGAGATTGGTATTTGTTTCACTTCATGAGCAATA 18909
QY	373 GCTTTTTCACTAACCGTGTGGTGTTTCCAAAGCTGGGAGTACAAGATATGCTTGCTT 432
DB	18910 GCTATTTTACATCAACCGTATTTGTTTCCAAAGCTGGGAGTACAAGATATGCTATTC 18969
QY	433 TT 434
DB	18970 TT 18971
	RESULT 10
AAZ99938	
ID	AAZ99938 standard; DNA; 2307 BP.
XX	
AC	AAZ99938;
XX	
DT	25-JUL-2000 (first entry)
XX	
DE	DNA encoding part of starch branching enzyme II clone 5A1.
XX	
XX	Wheat; starch branching enzyme II; SBEII; SBEII-1; starch;
XX	gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.
XX	
OS	Triticum aestivum.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..2307
FT	/*tag= a
FT	/product= "starch branching enzyme II"
FT	/transl_except= (pos: 2036..2038, aa: Xaa)
FT	/transl_except= (pos: 2051..2053, aa: Xaa)
FT	/transl_except= (pos: 2090..2092, aa: Xaa)
FT	/transl_except= (pos: 2096..2098, aa: Xaa)
FT	/transl_except= (pos: 2114..2116, aa: Xaa)
FT	/transl_except= (pos: 2147..2149, aa: Xaa)
FT	/transl_except= (pos: 2168..2170, aa: Xaa)
FT	/transl_except= (pos: 2174..2176, aa: Xaa)
FT	/transl_except= (pos: 2189..2191, aa: Xaa)
FT	/transl_except= (pos: 2267..2269, aa: Xaa)
FT	/transl_except= (pos: 2270..2272, aa: Xaa)
FT	/transl_except= (pos: 2306..2307, aa: Aan)
FT	/note= "Xaa is an unknown amino acid; the sequence
FT	contains 10 internal stop codons, but no termination
FT	codon"
XX	
PN	MO200015810-A1.
XX	
PD	23-MAR-2000.
XX	
PF	09-SEP-1999; 99MO-GB003011.
XX	
PR	10-SEP-1998; 98EP-00307337.
XX	

(PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.

Goldsbrough A, Collier S;

WPI: 2000-271446/23.

P-PSDB: AA84408.

DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch gelatinization onset and/or peak temperature.

Disclosure; Fig 10; 197pp; English.

The present sequence encodes a wheat starch branching enzyme II (SBEII) of a novel subclass of known SBEII genes, designated SBEII-1. The SBEII-1 genes are thought to have similar functional properties to the maize SBEIIb gene. Starch branching enzymes catalyse the formation of the alpha-1,6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-glucan chain to the same or another glucosyl chain. SBEII polypeptides can be used to alter the characteristics of a plant, in particular to alter starch so that it has an elevated gelatinization onset and/or peak temperature. Starch obtained from transgenic plants is useful in the preparation or processing a foodstuff, particularly bakery products

Sequence 2307 BP; 674 A; 440 C; 544 G; 635 T; 0 U; 14 Other;

Query Match
Best Local Similarity 9.3%; Score 125.6; DB 3; Length 2307;
Matches 140; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

264 TTTATGACATCTGAGACCAAGTATGTTTCACGAAACATGAGAAAGATGAATGATCATC 323
1508 TTTATGACATCTGAGACCAAGTATGTTTCACGAAACATGAGAAAGATGAATGATCATC 1567

324 CTCAAAAGAGAGATTGTTGTTTTCACCTTCACCTGAGACATAGCTTTTGGAC 383

1568 TTTGAAAAAGGGGACTGTGTTTGTTCACCTTCACCTGAGACATAGCTTTTGGAC 1627

384 TACCGTTGGGTTCACAGCTGGGAGATACAAAGTATGCTT 427

1628 TACCGGTTGGCTGTTTAAAGCTGGGAGATACAAAGTATGCTT 1671

RESULT 11

ADCC07807 standard; DNA; 2307 BP.

ADCC07807;

18-DEC-2003 (first entry)

Rice DNA sequence seq ID73 related to grain filling.

plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; carbohydrate degradation; plant grain; grain filling; corn; tomato; banana; canola; cotton; peanut; tobacco; sugarcane; wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain; gene; de; plant.

Oryza sativa.

WO2003000905-A2.

03-JAN-2003.

21-JUN-2002; 2002MO-IB002450.

22-JUN-2001; 2001US-0300112P.

26-SEP-2001; 2001US-0325277P.

20-DEC-2001; 2001US-0342327P.

(SYGN) SYNGENTA PARTICIPATIONS AG.

Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;

Glazebrook J, Katagiri F, Kreps J, Provart N, Riecke D;

WPI: 2003-229341/22.

P-PSDB: ADCC07808.

New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.

Claim 2; SEQ ID NO 73; 130pp; English.

This invention, in the area of plant biotechnology, relates to novel polynucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarcane, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/publishedpct_sequences.

Sequence 2307 BP; 608 A; 465 C; 620 G; 614 T; 0 U; 0 Other;

Query Match
Best Local Similarity 9.3%; Score 124.4; DB 9; Length 2307;
Matches 137; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

263 GTTATGACATCTGAGACCAAGTATGTTTCACGAAACATGAGAAAGATGAATGATCATC 322

2004 GTTATGACATCTGAGACCAAGTATGTTTCACGAAACATGAGAAAGATGAATGATCATC 2063

323 CCTCAAAGAGAGATTGTTGTTTTCACCTTCACCTGAGACATAGCTTTTGGAC 382

2064 CTTCAGAGAGAGATTGTTGTTTTCACCTTCACCTGAGACATAGCTTTTGGAC 2123

383 CTACCGTTGGGTTCACAGCTGGGAGATACAAAG 420

2124 CTATCGCGTGGTGTTTAAAGCTGGAAAGTACAAAG 2161

RESULT 12

AAZ99941 standard; DNA; 1120 BP.

AAZ99941;

25-JUL-2000 (first entry)

Nucleotide sequence of starch branching enzyme II clone B10.

Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2; gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.

Triticum aestivum.

WO200015810-A1.

23-MAR-2000.

09-SEP-1999; 99WO-GB003011.

10-SEP-1998; 98EP-00307337.

(PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.

XX Goldsbrough A, Colliver S;
XX WPI; 2000-271446/23.

XX DNA encoding wheat starch branching enzyme II isoforms, useful in
XX altering the characteristics of a plant, especially elevated starch
XX gelatinization onset and/or peak temperature.

PS Claim 4; Page 123-124; 197pp; English.

XX The present sequence represents a clone of wheat starch branching enzyme
XX II (SBEII), which is part of a novel subclass of known SBEII genes,
XX designated SBEII-1, subclass B. The specification also describes subclass
XX SBEII-2 sequences. The SBEII-1 genes are thought to have similar
XX functional properties to the maize SBEIIb gene. Starch branching enzymes
XX catalyse the formation of the alpha-1,6 linkages, creating branch points
XX in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage
XX followed by reattachment of the released alpha-1,4-glucan chain to the
XX same or another glucosyl chain. SBEII polypeptides can be used to alter
XX the characteristics of a plant, in particular to alter starch so that it
XX has an elevated gelatinisation onset and/or peak temperature. Starch
XX obtained from transgenic plants is useful in the preparation or
XX processing a foodstuff, particularly bakery products

SQ Sequence 1120 BP; 338 A; 208 C; 252 G; 308 T; 0 U; 14 Other;

Query Match 9.2%; Score 124.2; DB 3; Length 1120;

Best Local Similarity 79.5%; Pred. No. 5.2e-28;

Matches 147; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGCAGCAGTATGTTTCAACGGAACATGAGAAATAGATGATC 323
DB 325 TTTATGACATCTGAGCAGCAGTATGTTTCAACGGAACATGAGAAATAGATGATC 384
QY 324 CTCGAAAGAGAGATTTGTTTCACTTCCACTGAGCAATAGCTTTTGGAC 383
DB 385 TTGAAAAAGGGGACTGTGTTTGTTCACCTTCGAGTAGTATTTGCAC 444
QY 384 TACCGTGTGGTGTTCAGACCTGGAGATGACATGCTGCTTTTCACTTGTCCA 443
DB 445 TACCGGTTGGCTGTTTAAAGCTGGAGATGACATGCTGCTGAGCGCTGGA 504
QY 444 CCCTT 448
DB 505 CTCTT 509

RESULT 13

AAZ99940 standard; DNA; 1087 BP.

XX AAZ99940;
XX 25-JUL-2000 (first entry)
XX Nucleotide sequence of starch branching enzyme II clone B4.
XX Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2;
XX gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.
XX Triticum aestivum.
XX WO200015810-A1.
XX 23-MAR-2000.
XX 09-SEP-1999; 99WO-GB003011.
XX 10-SEP-1998; 98EP-00307337.

XX (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.

PI Goldsbrough A, Colliver S;
XX WPI; 2000-271446/23.

XX DNA encoding wheat starch branching enzyme II isoforms, useful in
XX altering the characteristics of a plant, especially elevated starch
XX gelatinization onset and/or peak temperature.

PS Claim 3; Page 123; 197pp; English.

XX The present sequence represents a clone of wheat starch branching enzyme
XX II (SBEII), which is part of a novel subclass of known SBEII genes,
XX designated SBEII-1, subclass C. The specification also describes subclass
XX SBEII-2 sequences. The SBEII-1 genes are thought to have similar
XX functional properties to the maize SBEIIb gene. Starch branching enzymes
XX catalyse the formation of the alpha-1,6 linkages, creating branch points
XX in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage
XX followed by reattachment of the released alpha-1,4-glucan chain to the
XX same or another glucosyl chain. SBEII polypeptides can be used to alter
XX the characteristics of a plant, in particular to alter starch so that it
XX has an elevated gelatinisation onset and/or peak temperature. Starch
XX obtained from transgenic plants is useful in the preparation or
XX processing a foodstuff, particularly bakery products

SQ Sequence 1087 BP; 336 A; 214 C; 235 G; 296 T; 0 U; 6 Other;

Query Match 9.2%; Score 124; DB 3; Length 1087;

Best Local Similarity 84.8%; Pred. No. 5.9e-28;

Matches 139; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGCAGCAGTATGTTTCAACGGAACATGAGAAATAGATGATC 323
DB 325 TTTATGACATCTGAGCAGCAGTATGTTTCAACGGAACATGAGAAATAGATGATC 384
QY 324 CTCGAAAGAGAGATTTGTTTCACTTCCACTGAGCAATAGCTTTTGGAC 383
DB 385 TTGAAAAAGGGGACTGTGTTTGTTCACCTTCGAGTAGTATTTGCAC 444
QY 384 TACCGTGTGGTGTTCAGACCTGGAGATGACATGCTGCTTTTCACTTGTCCA 443
DB 445 TACCGGTTGGCTGTTTAAAGCTGGAGATGACATGCTGCTGAGCGCTGGA 504

RESULT 14

ADC08218 standard; DNA; 2304 BP.

XX ADC08218;
XX 18-DEC-2003 (first entry)
XX Rice DNA sequence Seq ID523 related to grain filling.
XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
XX carbohydrate degradation; plant grain; grain filling; corn;
XX tomato; banana; cotton; peanut; sorghum; tobacco; sugarcane;
XX wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
XX gene; ds; plant.
XX Oryza sativa.
XX WO200300905-A2.
XX 03-JAN-2003.
XX 21-JUN-2002; 2002WO-1B002450.
XX 22-JUN-2001; 2001US-0300112P.
XX 26-SEP-2001; 2001US-0325277P.
XX 20-DEC-2001; 2001US-0342327P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Glazebrook J, Katagiri F, Krepe J, Provart N, Rieke D;
DR WPI, 2003-229341/22.
DR P-PSDB; ADC08219.
XX New plant genes encoding polypeptides having an activity involved in or
XX associated with the synthesis, metabolism or degradation of carbohydrates
XX in the plant grain useful in generating plants having improved
XX nutritional properties.

PS Claim 35; SEQ ID NO 523; 130pp; English.

CC This invention, in the area of plant biotechnology, relates to novel
CC polynucleotides comprising a nucleotide sequence encoding a protein which
CC is involved in or associated with the synthesis, metabolism or
CC degradation of carbohydrates in the plant grain and the expression of
CC which is up-regulated during grain filling. The plant is selected from
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
CC sugarcane, wheat, and rice. The invention may be useful for the
CC improvement of protein, oil, starch, fibre and moisture content of the
CC cereal grains. In addition, carbohydrate levels may be modified to a more
CC desirable level using the present invention. The present sequence is a
CC DNA sequence encoding a rice protein of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/publishedpct_sequences.

SQ Sequence 2304 BP; 610 A; 457 C; 620 G; 617 T; 0 U; 0 Other;

Query Match 9.2%; Score 123.4; DB 9; Length 2304;
Best Local Similarity 84.2%; Pred. No. 1.4e-27;
Matches 139; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGACACGATATGTTTCACGGAACATGAGAGATAGGATCATC 323

DB 1987 TTCATGACATCTGAGACACGATATGTTTCACGGAACATGAGAGATAGGATCATC 2046

QY 324 CTCGAAAGAGAGATTTGGTATTTGTTTCACTCCACGAGACATAGCTTTTGGAC 383

DB 2047 TTCGAGAGAGAGATTTGGTATTTGTTTCACTCCACGAGATATAGCTATTTGGAC 2106

QY 384 TACCGTGTGGGTGTTCCAAAGCTGGGAAGTACAGGTATGCTTG 428

DB 2107 TATCGCGTGGGTGTTTAAAGCTGGAAGTACAGATGTGCTTG 2151

RESULT 15

ADA71289

ID ADA71289 standard; DNA; 2655 BP.

AC ADA71289;

DT 20-NOV-2003 (first entry)

DE Rice gene, SEQ ID 4612.

XX plant; bacterial infection; fungal infection; viral infection; rice;

KW gene; ds.

OS Oryza sativa.

PN WO2003000898-A1.

PD 03-JAN-2003.

PF 22-JUN-2001; 2001WO-IB001105.

PR 22-JUN-2001; 2001WO-IB001105.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

PI Katagiri F, Quan S, Tao Y, Whitcham S, Xie Z, Zhu T, Zou G;
XX WPI, 2003-175290/17.
DR Identifying at least one gene involved in plant resistance or response to
XX pathogenic infection for conferring resistance or tolerance to a plant to
XX bacterial, fungal or viral infection by determining or detecting plant
XX gene expression.

PS Claim 6; SEQ ID NO 4612; 899pp; English.

CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

SQ Sequence 2655 BP; 714 A; 529 C; 680 G; 732 T; 0 U; 0 Other;

Query Match 9.2%; Score 123.4; DB 7; Length 2655;
Best Local Similarity 84.2%; Pred. No. 1.6e-27;
Matches 139; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGACACGATATGTTTCACGGAACATGAGAGATAGGATCATC 323

DB 2338 TTCATGACATCTGAGACACGATATGTTTCACGGAACATGAGAGATAGGATCATC 2397

QY 324 CTCGAAAGAGAGATTTGGTATTTGTTTCACTCCACGAGACATAGCTTTTGGAC 383

DB 2398 TTCGAGAGAGAGATTTGGTATTTGTTTCACTCCACGAGATATAGCTATTTGGAC 2457

QY 384 TACCGTGTGGGTGTTCCAAAGCTGGGAAGTACAGGTATGCTTG 428

DB 2458 TATCGCGTGGGTGTTTAAAGCTGGAAGTACAGATGTGCTTG 2502

Search completed: April 10, 2004, 04:00:09
Job time : 528.86 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 03:15:35 ; Search time 95.5669 Seconds
(without alignments)
7804.525 Million cell updates/sec

Title: US-09-508-377-10_COPY_10120_11463
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Scoring table:
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	27.5	2853	4	US-09-609-040-3
2	125.6	9.3	2446	4	US-09-731-166-9
3	120.6	9.0	2665	4	US-09-257-894-1
4	120.6	9.0	2720	4	US-09-731-166-11
5	120.6	9.0	2725	3	US-08-941-445A-14
6	91	6.8	3074	3	US-09-087-277-1
7	91	6.8	3074	4	US-09-658-499-1
8	58.4	4.3	2470	4	US-09-731-166-13
9	58.4	4.3	2487	4	US-09-257-894-19
10	58.4	4.3	2565	4	US-09-257-894-24
11	58.4	4.3	2763	3	US-08-941-445A-16
12	58.4	4.3	2772	4	US-09-257-894-12
13	55.4	4.1	414	4	US-09-257-894-2
14	54	4.0	2909	3	US-08-104-158-1
15	54	4.0	2909	4	US-09-609-040-1
16	54	4.0	3128	3	US-08-716-449-1
17	52	3.9	2087	4	US-09-257-894-9
18	52	3.9	2165	4	US-09-257-894-8
19	44	3.3	7218	1	US-08-232-463-14
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21	37.2	2.8	1230025	4	US-09-198-452A-1
22	35	2.6	746	3	US-09-328-111-105
23	34.8	2.6	164976	4	US-08-232-463-14
24	34.6	2.6	21784	4	US-08-916-421B-1
25	33.8	2.5	632	3	US-09-820-002-3
26	32.8	2.4	9916	4	US-09-385-982-177
27	32.8	2.4	9916	4	US-09-816-095-3

c	28	32.2	2.4	848	3	US-08-905-223-27	Sequence 27, Appl
c	29	32.2	2.4	848	4	US-09-247-155-27	Sequence 27, Appl
c	30	32.2	2.4	848	4	US-09-663-600A-27	Sequence 27, Appl
c	31	32.2	2.4	848	4	US-09-621-976-5	Sequence 5, Appl
c	32	32.2	2.4	28171	4	US-08-961-527-22	Sequence 22, Appl
c	33	32	2.4	2448	3	US-08-691-563C-53	Sequence 53, Appl
c	34	32	2.4	2448	4	US-09-374-766-53	Sequence 53, Appl
c	35	32	2.4	2448	4	US-08-979-847B-49	Sequence 49, Appl
c	36	32	2.4	22846	2	US-08-468-461-3	Sequence 3, Appl
c	37	32	2.4	22846	3	US-07-890-609-3	Sequence 3, Appl
c	38	32	2.4	640681	4	US-09-790-988-1	Sequence 1, Appl
c	39	31.8	2.4	234	4	US-09-107-532A-252	Sequence 252, App
c	40	31.8	2.4	364	4	US-09-621-976-17202	Sequence 17202, A
c	41	31.8	2.4	474	4	US-09-621-976-18033	Sequence 18033, A
c	42	31.8	2.4	796	4	US-08-956-171E-602	Sequence 602, App
c	43	31.8	2.4	1429	2	US-09-159-385-4	Sequence 4, Appl
c	44	31.8	2.4	1429	3	US-09-186-277-4	Sequence 4, Appl
c	45	31.8	2.4	1497	4	US-09-220-132-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1									
US-09-609-040-3									
Sequence 3, Application US/09609040									
Patent No. 6570066									
GENERAL INFORMATION:									
APPLICANT: Willmitzer, et al.									
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRAT									
TITLE OF INVENTION: CONCENTRATION AND COMPOSITION IN PLANTS									
FILE REFERENCE: 514413-3515.1									
CURRENT FILING DATE: 2000-06-30									
PRIOR APPLICATION NUMBER: PCT/EP92/00302									
PRIOR FILING DATE: 1992-02-11									
NUMBER OF SEQ ID NOS: 4									
SOFTWARE: PatentIn version 3.0									
SEQ ID NO 3									
LENGTH: 2853									
TYPE: DNA									
ORGANISM: Trifolium aestivum									
FEATURE:									
NAME/KEY: CDS									
LOCATION: (313)..(2499)									
OTHER INFORMATION: BRANCHING ENZYME									
US-09-609-040-3									
Query Match									
Best Local Similarity 100.0%; Pred. No. 8.6e-110; Length 2853;									
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	961	GAACATCCGATGACACAGGCGGCTCTTTCTGGTGTACACTCCGACAGACTGCG	1020						
Db	2419	GAACATCCGATGACACAGGCGGCTCTTTCTGGTGTACACTCCGACAGACTGCG	2478						
Qy	1021	GTCGTGTATGCCCTTACAGAGTAAGACAGAGGCTTTTACAGAGCAAGAGAA	1080						
Db	2479	GTCGTGTATGCCCTTACAGAGTAAGACAGAGGCTTTTACAGAGCAAGAGAA	2538						
Qy	1081	CTCCAGAGAGCTCGTGTATGTCGAGACGAGCGGCGGAGGCTCTCCAG	1140						
Db	2539	CTCCAGAGAGCTCGTGTATGTCGAGACGAGCGGCGGAGGCTCTCCAG	2598						
Qy	1141	CGCCATGACTGGAGGGAGTGTGCTCTTCCCAATGCCAGAGAGAGATGATAG	1200						
Db	2599	CGCCATGACTGGAGGGAGTGTGCTCTTCCCAATGCCAGAGAGAGATGATAG	2658						
Qy	1201	GTAAGTTTGTGTAGCGCTGAAAGAAATGAGCGGCTGGGTGTTGTGCTGCA	1260						
Db	2659	GTAAGTTTGTGTAGCGCTGAAAGAAATGAGCGGCTGGGTGTTGTGCTGCA	2718						
Qy	1261	CTGAACCTCTCTATCTGTGACATATCCCGGCTGTTTGTATATATACTAATATG	1320						

Mon Apr 12 10:24:22 2004

us-09-508-377-10_copy_10120_11463.rni

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Db 2719 CTGAACTCTCTCCTATCTTGCACATTCGCCGTGTTTTGTACTATATACTAATATG 2778

Qy 1321 CCCGTGCGCT 1330

Db 2779 CCGTGGCGCT 2788

```

RESULT 2
US-09-731-166-9
Sequence 9, Application US/09731166
Patent No. 6639126
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccarides
FILE REFERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 2446
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: SBE11a
NAME/KEY: CDS
LOCATION: (2)...(2446)
US-09-731-166-9

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		9.3%;	Score 125.6;	DB 4;	length 2446;
		Best Local Similarity 79.3%;	Pred. No. 3.5e-30;		
		Matches 149;	Conservative 0;	Mismatches 39;	Indels 0; Gaps 0;
QY	262	AGTTTATGACATCTGAGGACCAAGTATGTTTTCACGGAACATGAGGAAGATTAAGTGATCA	321		
Db	2118	AATTCATGACATCTGATCATCTCATATGATATACGGAACATGAGGAGATTAAGGATCA	2177		
QY	322	TCCCAAAAGAGAGAGATTGGATTTGTTTTCACCTTCCATCGAGAGCAATAGCTTTTGTG	381		
Db	2178	TCTTTGAGAGAGAGAGATTGGTCTTTCGTTTCACCTTCCATCGAGAGCAATAGCTTTTGTG	223		
QY	382	ACTACCGTGGTGGTGTTCCAAAGCCTGGGAAGTACAAAGTATGCTTGCCTTTCAATTGTC	441		
Db	2238	ACTATCGGTTGGTGGTGTTCAAAGCCTGGGAAGTACAAAGTATGCTTTAGATTCTGACGATG	2297		
QY	442	CACCCCTTC	449		
Db	2298	GCCCTTTTC	2305		

RESULT 3
 US-09-257-894-1
 Sequence 1, Application US/09257894
 Patent No. 6376749
 GENERAL INFORMATION:
 APPLICANT: Broglie, Karen E.
 APPLICANT: Klein, Theodore M.
 APPLICANT: Hubbard, Natalie L.
 APPLICANT: Lightner, Jonathan E.
 TITLE OF INVENTION: No. 6376749e1 Starches via Modification of
 TITLE OF INVENTION: Expression of Starch Biosynthesis
 TITLE OF INVENTION: Enzyme Genes
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: E. I. du Pont de Nemours and Company
 STREET: 1007 Market Street
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Query Match	9.0%;	Score 120.6;	DB 4;	Length 2665;
Best Local Similarity	82.6%;	Pred. No. 1.6e-28;		
Matches 138;	Conservative 0;	Mismatches 29;	Indels 0;	Gaps 0;
QY	262	AGTTATGACATCTGAGCACCAGTATGTTCCAGGAAAACATGAGAGATTAAGTGATCA	321	
Db	2162	AATTCATGACATCTGATACACCGATATATTTCCCGAAACATGAGAGAGATTAAGTGATTG	2221	
QY	322	TCTCTCAAAAGAGGAGATTGGTATTGTTTCAACTTCACATCGAAGCATAGCTTTTGG	381	
Db	2222	TGTTTCGAAAAGGAGATTGGTATTGTTGTTCAACTTCACATCGAACAACGCTATTTTG	2281	
QY	382	ACTACCGGTGGGNGTTCCAAGCTGGGAAGTCAAGATAGCTTG	428	
Db	2282	ACTACCGTATTGGTTGTCGAAAGCTGGGAGCTATTAAGTGATCTTG	2328	

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RESULT 4
US-03-731-166-11
; Sequence 11, Application US/09731166
; Patent No. 6639126
;
GENERAL INFORMATION:
;
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccharides
FILE REFERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11
;
; LENGTH: 2720
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature

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LOCATION: (0)...(0)
OTHER INFORMATION: SBEID
OTHER INFORMATION: Genbank Accession No. 6639126 AF072725
NAME/KEY: CDS
LOCATION: (101)...(2500)
US-09-731-166-11

Query Match 9.0%; Score 120.6; DB 4; Length 2720;
Best Local Similarity 82.6%; Pred. No. 1.6e-28;
Matches 138; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 262 AGTTTATGACATCTGACGACCGATGTTTCCAGGAAATAGAGAAATAGGATGATCA 321
DB 2184 AATTCATGACATCTGATCAACGATATTTCCCGAAACATGAGGAGATTAAGGTATTTG 2243
QY 322 TCCTCAAAAGAGAGATTTGGTATTTGTTTCAACTTCAGTGAACAATAGCTTTTGG 381
DB 2244 TGTTCGAAAAGGAGATTTGGTATTTGTTTCAACTTCAGTGAACAACAAGCTATTTTG 2303
QY 382 ACTACCGTGTGGGTGTTCCAAAGCTGGGAGTACAAAGGTATGCTTG 428
DB 2304 ACTACCGTATTTGTTGTGCAAAAGCTGGGAGTATTAAGGTGCTTG 2350

RESULT 5

US-08-941-445A-14
Sequence 14, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanning
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2725 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Zea mays
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 91..264
FEATURE:

NAME/KEY: mat_peptide
LOCATION: 265..2487
FEATURE:
NAME/KEY: CDS
LOCATION: 91..2490
US-08-941-445A-14

Query Match 9.0%; Score 120.6; DB 3; Length 2725;
Best Local Similarity 82.6%; Pred. No. 1.6e-28;
Matches 138; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 262 AGTTTATGACATCTGACGACCGATGTTTCCAGGAAATAGAGAAATAGGATGATCA 321
DB 2174 AATTCATGACATCTGATCAACGATATTTCCCGAAACATGAGGAGATTAAGGTATTTG 2233
QY 322 TCCTCAAAAGAGAGATTTGGTATTTGTTTCAACTTCAGTGAACAATAGCTTTTGG 381
DB 2234 TGTTCGAAAAGGAGATTTGGTATTTGTTTCAACTTCAGTGAACAACAAGCTATTTTG 2293
QY 382 ACTACCGTGTGGGTGTTCCAAAGCTGGGAGTACAAAGGTATGCTTG 428
DB 2294 ACTACCGTATTTGTTGTGCAAAAGCTGGGAGTATTAAGGTGCTTG 2340

RESULT 6

US-09-087-277-1
Sequence 1, Application US/09087277B
Patent No. 6169226
GENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNODI, Jamsheed
APPLICANT: LARSSON, Claas-Tomas
APPLICANT: LARSSON, Hakan
TITLE OF INVENTION: SPARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism:belli gene
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
OTHER INFORMATION: (potato)
FEATURE:
NAME/KEY: CDS
LOCATION: (189)..(2825)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (189)..(332)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
OTHER INFORMATION: n wherein n = A, C, G or T.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
OTHER INFORMATION: or Phe.

FEATURE: /
NAME/KEY: misc feature /
LOCATION: (1404)..(1406) /
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe. /
FEATURE: /
NAME/KEY: misc feature /
LOCATION: (1428)..(1430) /
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr. /
FEATURE: /
NAME/KEY: misc feature /
LOCATION: (1896)..(1898) /
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys /
OTHER INFORMATION: or Phe. /
FEATURE: /
NAME/KEY: misc feature /
LOCATION: (2154)..(2156) /
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro. /
US-09-087-277-1

Query Match /
Best Local Similarity 67.8%; Score 91; DB 3; Length 3074; /
Matches 127; Conservative 0; Mismatches 60; Indels 0; Gaps 0; /

QY 262 AGTTATGACATCTGAGCACCAGTAGTGTTCACGGAACATGAGGAAGATAGGTATCA 321 /
DB 2449 AGTTATGACCTCAGAACACAGTTCATATCAGAAAGATGAGAGATAGATGATG 2508 /
QY 322 TCCTCAAAAGAGAGATTGTATTTTTCACACTCCACTGAGCATAGCTTTTTC 381 /
DB 2509 TATTGAAAAAGAGAACTAGTTTTCCTTTAATTTTCACTGACAAAAAGCTATTTCAG 2568 /
QY 382 ACTACCGTGTGGGTGTTCAGAGCCTGGAGATACAGAGTATGCTTTTTCATTGTC 441 /
DB 2569 ACTATGCGATAGGCTGCTGAGAGCTGGAATAATCAAGTTGCTTGACTCAGATGATC 2628 /
QY 442 CACCTT 448 /
DB 2629 CACTTT 2635 /

RESULT 7 /
US-09-658-499-1 /
Sequence 1, Application US/09658499 /
Patent No. 6469231 /
GENERAL INFORMATION: /
APPLICANT: EK, BO /
APPLICANT: KHOSNOODI, Jamshid /
APPLICANT: LARSSON, Claes-Tomas /
APPLICANT: LARSSON, Hakan /
APPLICANT: RASK, Lars /
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO /
FILE REFERENCE: 003300-486 /
CURRENT APPLICATION NUMBER: US/09/658,499 /
CURRENT FILING DATE: 2000-09-08 /
PRIOR APPLICATION NUMBER: 09/087,277 /
PRIOR FILING DATE: 1998-05-29 /
PRIOR APPLICATION NUMBER: PCT/SE96/01558 /
PRIOR FILING DATE: 1996-11-28 /
PRIOR APPLICATION NUMBER: SE 9504272-7 /
PRIOR FILING DATE: 1995-11-29 /
PRIOR APPLICATION NUMBER: SE 9601506-0 /
PRIOR FILING DATE: 1996-04-19 /
NUMBER OF SEQ ID NOS: 4 /
SOFTWARE: PatentIn Ver. 2.0 /
SEQ ID NO 1 /
LENGTH: 3074 /
TYPE: DNA /
ORGANISM: Unknown /
FEATURE: /
OTHER INFORMATION: Description of Unknown Organism: bell gene /
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum /
OTHER INFORMATION: (potato) /
NAME/KEY: CDS /

LOCATION: (189)..(2825) /
NAME/KEY: sig_peptide /
LOCATION: (189)..(332) /
NAME/KEY: mat_peptide /
LOCATION: (333)..(2825) /
NAME/KEY: misc_feature /
LOCATION: (92)..(2156) /
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are /
OTHER INFORMATION: n wherein n = A, C, G or T. /
NAME/KEY: misc_feature /
LOCATION: (285)..(287) /
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val /
OTHER INFORMATION: or Phe. /
NAME/KEY: misc_feature /
LOCATION: (1404)..(1406) /
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe. /
NAME/KEY: misc_feature /
LOCATION: (1428)..(1430) /
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr. /
NAME/KEY: misc_feature /
LOCATION: (1896)..(1898) /
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys /
OTHER INFORMATION: or Phe. /
NAME/KEY: misc_feature /
LOCATION: (2154)..(2156) /
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro. /
US-09-658-499-1

Query Match /
Best Local Similarity 67.8%; Score 91; DB 4; Length 3074; /
Matches 127; Conservative 0; Mismatches 60; Indels 0; Gaps 0; /

QY 262 AGTTATGACATCTGAGCACCAGTAGTGTTCACGGAACATGAGGAAGATAGGTATCA 321 /
DB 2449 AGTTATGACCTCAGAACACAGTTCATATCAGAAAGATGAGAGATAGATGATG 2508 /
QY 322 TCCTCAAAAGAGAGATTGTATTTTTCACACTCCACTGAGCATAGCTTTTTC 381 /
DB 2509 TATTGAAAAAGAGAACTAGTTTTCCTTTAATTTTCACTGACAAAAAGCTATTTCAG 2568 /
QY 382 ACTACCGTGTGGGTGTTCAGAGCCTGGAGATACAGAGTATGCTTTTTCATTGTC 441 /
DB 2569 ACTATGCGATAGGCTGCTGAGAGCTGGAATAATCAAGTTGCTTGACTCAGATGATC 2628 /
QY 442 CACCTT 448 /
DB 2629 CACTTT 2635 /

RESULT 8 /
US-09-731-166-13 /
Sequence 13, Application US/09731166 /
Patent No. 6639126 /
GENERAL INFORMATION: /
APPLICANT: Sewalt, Vincent J. H. /
APPLICANT: Singletary, George W. /
TITLE OF INVENTION: Production of Modified Polysaccharides /
FILE REFERENCE: 35718/206348 /
CURRENT APPLICATION NUMBER: US/09/731,166 /
CURRENT FILING DATE: 2000-12-06 /
PRIOR APPLICATION NUMBER: 60/169,993 /
PRIOR FILING DATE: 1999-12-06 /
NUMBER OF SEQ ID NOS: 16 /
SOFTWARE: FastSeq for Windows Version 4.0 /
SEQ ID NO 13 /
LENGTH: 2470 /
TYPE: DNA /
ORGANISM: Zea mays /
FEATURE: /
NAME/KEY: misc_feature /
LOCATION: (0)..(0) /
OTHER INFORMATION: SBE1 -- Genbank Accession No. 6639126 217959 /
NAME/KEY: CDS /

LOCATION: (2)...(2470)
US-09-731-166-13

Query Match 4.3%; Score 58.4; DB 4; Length 2470;
Best Local Similarity 56.9%; Pred. No. 2.8e-08;
Matches 107; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 301 ATGAGAGATTAAGTATGATCATCTCAAAAGAGAGATTGGTATTGTTTCAACTTCC 360
DB 1995 ACGATGAGAAAAGGTTATGCTCTTGAACGTGAGATTAGTTTGTTCATTCC 2054
QY 361 ACTGAGCAATAGCTTTTGTACTACCGTGTGGGTTCAGCTGGGAAGTACAAG 420
DB 2055 ATCCCAAGAAAACCTACGAGGGCTACAAAGTGGGATGCGATTGCTGGGAAATACAGAG 2114
QY 421 TAGCTTGCCTTTTCATTGTCACCCCTTACCAAGTAGGTTAGTGGGGCTTCTCAACT 480
DB 2115 TAGCCCTGACTCTGATGCTGTGCTTGGTGGATGAGATGGAAGAGTTGGCCACGAGCTGG 2174
QY 481 TTTAATTC 488
DB 2175 ATCACTTC 2182

RESULT 9

US-09-257-894-19/c
Sequence 19, Application US/09257894
Patent No. 6376749

GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2487 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-257-894-19

Query Match

4.3%; Score 58.4; DB 4; Length 2487;

Best Local Similarity 56.9%; Pred. No. 2.8e-08;
Matches 107; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 301 ATGAGAGATTAAGTATGATCATCTCAAAAGAGAGATTGGTATTGTTTCAACTTCC 360
DB 380 ACGATGAGAAAAGGTTATGCTCTTGAACGTGAGATTAGTTTGTTCATTCC 321
QY 361 ACTGAGCAATAGCTTTTGTACTACCGTGTGGGTTCAGCTGGGAAGTACAAG 420
DB 320 ATCCCAAGAAAACCTACGAGGGCTACAAAGTGGGATGCGATTGCTGGGAAATACAGAG 261
QY 421 TAGCTTGCCTTTTCATTGTCACCCCTTACCAAGTAGGTTAGTGGGGCTTCTCAACT 480
DB 260 TAGCCCTGACTCTGATGCTGTGCTTGGTGGATGAGATGGAAGAGTTGGCCACGAGCTGG 201
QY 481 TTTAATTC 488
DB 200 ATCACTTC 193

RESULT 10

US-09-257-894-24
Sequence 24, Application US/09257894
Patent No. 6376749

GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-257-894-24

Query Match 4.3%; Score 58.4; DB 4; Length 2565;
Best Local Similarity 56.9%; Pred. No. 2.9e-08;
Matches 107; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 301 ATGAGAGATTAAGTATGATCATCTCAAAAGAGAGATTGGTATTGTTTCAACTTCC 360

Db 1997 ACCATGAGGAAAGATATGCTTTTGAAGTGAGATTGATTTGTTTCAATTCC 2056
QY 361 ACTGAGACATACCTTTTGTGACTACCGTGTGGGTGTTCCAGCCTGGAGTACAG 420
Db 2057 ATCCCAAGAAACTTACGAGGCTACAAAGTGGATGCGATTGCTGGAAATACAG 2116
QY 421 TATGCTGCTTTTCAATGTCACCTTTCACAGTAGGGTTAGGGGCTTTCACACT 480
Db 2117 TAGCCCTGAGCTGTGATGCTGTGTCTTCCGTGACATGAGAGATTGGCAGCAGCTGG 2176
QY 481 TTTAATTC 488
Db 2177 ATCACTTC 2184

RESULT 11
US-08-941-445A-16
Sequence 16, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
TITLE OF INVENTION: Search Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Zea mays
FEATURE:
NAME/KEY: translt_peptide
LOCATION: 2..190
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 191..2467
FEATURE:
NAME/KEY: CDS
LOCATION: 2..2470
US-08-941-445A-16

Query Match

4.3%; Score 58.4; DB 3; Length 2763;

Best Local Similarity 56.9%; Pred. No. 3.1e-08;
Matches 107; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 301 ATGAGAGAGATAGGATGATCATCTCAAAAGAGAGATTTGGTATTTGTTCACTCC 360
Db 1995 ACGATGAGGAAAGATTATGTCTTTGAACGTGGAGATTAGTTTGTTCATTTCC 2054
QY 361 ACTGAGCAATGCTTTTGTACTACCGTGTGGTGTTCACAGCCTGGAGTACAG 420
Db 2055 ATCCCAAGAAACTTACGAGGCTACAAAGTGGATGCGATTTGCCGGGAAATACAG 2114
QY 421 TATGCTGCTTTTCAATGTCACCTTTCACAGTAGGGTTAGGGGCTTTCACACT 480
Db 2115 TAGCCCTGAGCTGTGATGCTGTGTCTTCCGTGACATGAGAGATTGGCAGCAGCTGG 2174
QY 481 TTTAATTC 488
Db 2175 ATCACTTC 2182

RESULT 12
US-09-257-894-12
Sequence 12, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749e1 Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-773-0164
TELEFAX: 302-992-4926
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 49..2580
US-09-257-894-12

Query Match

4.3%; Score 58.4; DB 4; Length 2772;
Best Local Similarity 56.9%; Pred. No. 3.1e-08;

Mon Apr 12 10:24:22 2004

us-09-508-377-10_copy_10120_11463.rml

Page 7

Matches 107; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 301 ATGAGGAATATAGTGTATCTCCCAAGAGAGATTGGTATTTGTTCACTTCC 360
Db 2108 ACGATGAGGAAAGGTTATGTCTTGAACGTGAGATTAGTTTGTTCATTTCC 2167
QY 361 ACTGAGCAATAGCTTTTGTACTACCGTGTGGGTGTTCCAAAGCTGGAGATACAG 420
Db 2168 ATCCCAAGAAACTTACGAGGGCTCAAAAGTGGATGCCATTGGCTGGAAATACAG 2227
QY 421 TATGCTTCCTTTTCAATGTCCACCTTCACAGTAGGGTTAGTGGGGCTTTACACT 480
Db 2228 TAGCCCTGAGCTGTATGTCTGTCTTCGTGACATGGAAGATTGGCCACGAGCTG 2287
QY 481 TTTAATTC 488
Db 2288 ATCACTTC 2295

RESULT 13

US-09-257-894-2/C
Sequence 2, Application US/09257894

Patent No. 6376749

GENERAL INFORMATION:

APPLICANT: Broglie, Karen E.

APPLICANT: Klein, Theodore M.

APPLICANT: Hubbard, Natalie L.

APPLICANT: Lightner, Jonathan E.

TITLE OF INVENTION: No. 6376749el Starches via Modification of

TITLE OF INVENTION: Expression of Starch Biosynthesis

TITLE OF INVENTION: Enzyme Genes

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. du Pont de Nemours and Company

STREET: 1007 Market Street

CITY: Wilmington

STATE: Delaware

COUNTRY: USA

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Microsoft Windows 95

SOFTWARE: Version 7.0A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/257,894

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/091,052

FILING DATE: JUNE 10, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Majarian, William R.

REGISTRATION NUMBER: 41,173

REFERENCE/DOCKET NUMBER: BB-1066-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-992-4926

TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 414 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-257-894-2

Query Match

Best Local Similarity 4.1%; Score 55.4; DB 4; Length 414;

Matches 65; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

348 GTTTCACCTTCACGTGAGCAATAGCTTTTGTACTACCGTGTGGGTGTTCCAGCCT 407

Db 414 GTGTTCACCTTCACGTGCAACACAGCTATTGTGACTACCGTATTGGTTGAAAAAGCCT 355

QY 408 GGGAGATCAAGGTATGCTTG 428

Db 354 GGGGTGTATAGAGTGTCTTG 334

RESULT 14

US-08-104-158-1

Sequence 1, Application US/08104158

Patent No. 6215042

GENERAL INFORMATION:

APPLICANT: Wilmltzer, Lothar

APPLICANT: Sonnewald, Uwe

APPLICANT: Kossmann, Jens

APPLICANT: Mueller-Roebert, Bernd

APPLICANT: Visser, Richard Gerardus Franciscus

APPLICANT: Jacobsen, Evert

TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT

TITLE OF INVENTION: CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE

TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS

TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ostroienk, Faber, Gerb & Soffen

STREET: 1180 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-8403

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/104,158

FILING DATE: 13-AUG-1993

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP PCT/EP92/00302

FILING DATE: 11-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 41 04 782.6

FILING DATE: 13-FEB-1991

ATTORNEY/AGENT INFORMATION:

NAME: Wellman, Edward A.

REGISTRATION NUMBER: 24,735

REFERENCE/DOCKET NUMBER: PA-1996 PCT (951-91)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-382-0700

TELEFAX: 212-382-0888

TELEX: 236925

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2909 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Solanum tuberosum cv. Desiree

STRAIN: Desiree

DEVELOPMENTAL STAGE: growing tuber

TISSUE TYPE: tuber

CELL TYPE: total tuber

IMMEDIATE SOURCE:

LIBRARY: cDNA of total tuber mRNA in pUC 19 (Hinc II)

FEATURE:

NAME/KEY: CDS

LOCATION: 2..1699

OTHER INFORMATION: /note= "for Branching enzyme I
OTHER INFORMATION: (partial) truncated protein: 97,11 % identity to
OTHER INFORMATION: active potato branching enzyme"
US-08-104-158-1

Query Match 4.0%; Score 54; DB 3; Length 2909;
Best Local Similarity 58.9%; Pred. No. 8.6e-07;
Matches 93; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 264 TTTATACATCTGAGCACCAGTATGTTTCACGGAAACATGAGAGATAGGTATCATC 323
DB 1866 TTCCGTCATCAGAGAAACAGATAGTAGCAGCATGATGATGATGATGATGATG 1925
QY 324 CTCGAAAGAGAGATTTGATTTGTTTCACTTCAGCTGGAGCAATAGCTTTTGAC 383
DB 1926 TTGAAAGTGCTGACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1985
QY 384 TACCGTGTGGTGTTCAGAGCTGGAGAGTACAGGT 421
DB 1986 TATAAGTTGATGTGACTTGCCAGGAGAGTACAGAGT 2023

RESULT 15

US-09-609-040-1
; Sequence 1, Application US/09609040
; Patent No. 6570066
; GENERAL INFORMATION:
; APPLICANT: Wilmilizer, et al.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE
; FILE REFERENCE: 514413-3515.1
; CURRENT APPLICATION NUMBER: US/09/609,040
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: PCT/EP92/00302
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO. 1
; LENGTH: 2909
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1699)
; OTHER INFORMATION: BRANCHING ENZYME
US-09-609-040-1

Query Match 4.0%; Score 54; DB 4; Length 2909;
Best Local Similarity 58.9%; Pred. No. 8.6e-07;
Matches 93; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 264 TTTATACATCTGAGCACCAGTATGTTTCACGGAAACATGAGAGATAGGTATCATC 323
DB 1866 TTCCGTCATCAGAGAAACAGATAGTAGCAGCATGATGATGATGATGATGATG 1925
QY 324 CTCGAAAGAGAGATTTGATTTGTTTCACTTCAGCTGGAGCAATAGCTTTTGAC 383
DB 1926 TTGAAAGTGCTGACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1985
QY 384 TACCGTGTGGTGTTCAGAGCTGGAGAGTACAGGT 421
DB 1986 TATAAGTTGATGTGACTTGCCAGGAGAGTACAGAGT 2023

Search completed: April 10, 2004, 14:13:17
Job time: 100.567 secs

Mon Apr 12 10:24:22 2004

us-09-508-377-10_copy_10120_11463.rmpb

Page 1

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 10:02:36 ; Search time 474.681 Seconds
(without alignments)
10621.793 Million cell updates/sec

Title: US-09-508-377-10_COPY_10120_11463

Perfect score: 1344

Sequence: 1 ttgaatcgcggtggtcga.....tgcgtcaccggtgaatcc 1344

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2475585 seqs, 1875730760 residues

Total number of hits satisfying chosen parameters: 4951170

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1333	99.2	11476	12	US-10-434-893A-3
2	370	27.5	1119	15	US-10-260-238-3410
3	263.6	19.6	2554	12	US-10-434-893A-1
4	122.6	9.1	3039	9	US-09-792-127-1
5	122.6	9.1	3039	9	US-09-792-127-3
6	122.4	9.1	1667	15	US-10-260-238-3480
7	120.6	8.9	636	15	US-10-260-238-3553
8	119.6	8.0	2780	12	US-10-434-893A-2
9	107.2	8.0	1642	15	US-10-260-238-1027
10	97	7.2	602	9	US-09-770-149-955
11	97	7.2	2418	9	US-09-938-842A-872
12	97	7.2	2418	11	US-09-938-842A-872
13	95.4	7.1	2529	14	US-10-056-454A-17
14	92.6	6.9	2975	14	US-10-056-454A-13
15	91.6	6.8	1867	12	US-10-425-114-8329

16	91.6	6.8	5164	12	US-10-424-599-130849	Sequence 130849, A
17	91	6.8	1255	14	US-10-171-008-3	Sequence 3, Appl1
18	91	6.8	2576	14	US-10-056-454A-16	Sequence 16, Appl1
19	91	6.8	2578	14	US-10-056-454A-19	Sequence 19, Appl1
20	91	6.8	3074	14	US-10-254-534-1	Sequence 1, Appl1
21	91	6.8	3231	14	US-10-056-454A-18	Sequence 18, Appl1
22	89.4	6.7	3003	14	US-10-056-454A-12	Sequence 12, Appl1
23	89.4	6.7	3033	14	US-10-056-454A-14	Sequence 14, Appl1
24	84.4	6.3	359	15	US-10-393-840-264	Sequence 264, App
25	84.4	6.3	2577	9	US-09-938-842A-337	Sequence 337, App
26	84.4	6.3	2577	11	US-09-938-842A-337	Sequence 337, App
27	58.4	4.3	2324	12	US-10-425-114-3212	Sequence 3212, A
28	58.4	4.3	2551	15	US-10-357-954A-2	Sequence 36, Appl1
29	55.2	4.1	2913	12	US-10-235-192A-36	Sequence 442, App
30	55.2	4.1	2913	12	US-10-342-887-442	Sequence 2148, App
31	55.2	4.1	2955	9	US-09-880-107-2148	Sequence 30, Appl1
32	55.2	4.1	2955	10	US-09-880-107-2148	Sequence 107, App
33	55.2	4.1	2958	12	US-10-262-811-107	Sequence 92, Appl1
34	55.2	4.1	2994	14	US-10-084-817-92	Sequence 134, App
35	55.2	4.1	3075	14	US-10-240-965-135	Sequence 1616, App
36	54.8	4.1	1380	12	US-10-102-524-1616	Sequence 141092, A
37	54	4.0	2443	15	US-10-397-954A-1	Sequence 25407, A
38	53.6	4.0	2115	15	US-10-369-493-25407	Sequence 27656, A
39	53	3.9	2638	15	US-10-369-493-27656	Sequence 11503, A
40	50.4	3.8	897	12	US-10-425-114-11503	Sequence 54140, A
41	48.6	3.6	358	12	US-10-085-783A-54140	Sequence 54140, A
42	48.4	3.6	358	15	US-10-242-535A-54140	Sequence 54106, A
43	48.4	3.6	489	12	US-10-085-783A-14106	Sequence 14106, A
44	48.4	3.6	489	15	US-10-242-535A-14106	Sequence 14106, A
45	48.4	3.6	489	15	US-10-242-535A-14106	Sequence 14106, A

ALIGNMENTS

RESULT 1
US-10-434-893A-3
; Sequence 3, Application US/10434893A
; Publication No. US2004006083A1
; GENERAL INFORMATION:
; APPLICANT: Ahmed Regina
; APPLICANT: Matthew Kennedy Morell
; TITLE OF INVENTION: Sadequr Rahman
; TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and st
; FILE REFERENCE: 68425
; CURRENT APPLICATION NUMBER: US/10/344,893A
; CURRENT FILING DATE: 2003-05-09
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 3
; LENGTH: 11476
; TYPE: DNA
; ORGANISM: Aegilops tauschii
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1) (11476)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; OTHER INFORMATION: SSBETa gene
US-10-434-893A-3

Query Match 99.2% Score 1333; DB 12; Length 11476;
Best Local Similarity 99.9% Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTGATATCGTGTGATGCAAGAGTTCATCGAGCATGAGCATCTTGAAGAAATATG 60
DB 10132 TTGATATCGTGTGATGCAAGAGTTCATCGAGCATGAGCATCTTGAAGAAATATG 10191
QY 61 GGGATATGTCATGTTGTTCTTTGTTGATATCAACATGACATTTAAAGCTGCTCTTC 120
DB 10192 GGGATATGTCATGTTGTTCTTTGTTGATATCAACATGACATTTAAAGCTGCTCTTC 10251

QY 121 AAGTGTAAAAAAGTGTAAATTAATTCCTGTAAATGAGTAAAGTGTGCAAGGCG 180
Db 10252 AAGTGTAAAAAAGTGTAAATTAATTCCTGTAAATGAGTAAAGTGTGCAAGGCG 10311
QY 181 AAGTGTAAATGCTTTTACCAAAACATATTTTCTTAAGTGTGTGTATGTATACATATAC 240
Db 10312 AAGTGTAAATGCTTTTACCAAAACATATTTTCTTAAGTGTGTGTATGTATACATATAC 10371
QY 241 CAGACTGACATGTAACTGCAAGTTATGACATGTGACACCAAGTATGTTTCAAGAAAC 300
Db 10372 CAGACTGACATGTAACTGCAAGTTATGACATGTGACACCAAGTATGTTTCAAGAAAC 10431
QY 301 ATGAGAAAGTAAAGTATCATCTC-AAAAGAGATTTGATTTGTTTCAACTC 359
Db 10432 ATGAGAAAGTAAAGTATCATCTC-AAAAGAGATTTGATTTGTTTCAACTC 10491
QY 360 CACTGAGCAATAGCTTTTGTACTACCGTGTGGTGTCCAAAGCTGGAGTACAG 419
Db 10492 CACTGAGCAATAGCTTTTGTACTACCGTGTGGTGTCCAAAGCTGGAGTACAG 10551
QY 420 GTATGCTGCTTTTCAATGTCCACCTTCAACATGAGGTTAGTGGGGCTTCTACAC 479
Db 10552 GTATGCTGCTTTTCAATGTCCACCTTCAACATGAGGTTAGTGGGGCTTCTACAC 10611
QY 480 TTTTAATTCACATGATAGATTTGTGTGCGAGCTATCAATATAAGATAGAGGT 539
Db 10612 TTTTAATTCACATGATAGATTTGTGTGCGAGCTATCAATATAAGATAGAGGT 10671
QY 540 AATTTGTAAGAAAGATTTGCTCGAGCTGTGTAGCCATAGAGGTTGTTCTTAA 599
Db 10672 AATTTGTAAGAAAGATTTGCTCGAGCTGTGTAGCCATAGAGGTTGTTCTTAA 10731
QY 600 GCCCGAAGACATACCATTCATTAATCTACTTAAGTGTGTTCAATCTTAT 659
Db 10732 GCCCGAAGACATACCATTCATTAATCTACTTAAGTGTGTTCAATCTTAT 10791
QY 660 GCTCAGTGTGACTGCTTAATTAATGACATATTTCCGAATCTACCTCAACCTCAG 719
Db 10792 GCTCAGTGTGACTGCTTAATTAATGACATATTTCCGAATCTACCTCAACCTCAG 10851
QY 720 CAGTTTAGACAGCCCATTTGACAAATGGCTGGTGTGTAGTGTGACAGTTTC 779
Db 10852 CAGTTTAGACAGCCCATTTGACAAATGGCTGGTGTGTAGTGTGACAGTTTC 10911
QY 780 TGTATTTCTTAATCAGGTGCTTGAATCTGACATGCACTCTTGTGTGATTCAGCA 839
Db 10912 TGTATTTCTTAATCAGGTGCTTGAATCTGACATGCACTCTTGTGTGATTCAGCA 10971
QY 840 GGTGTGATCATGATGTGACTTCAACACCGTAAGTGTGGGCTCAGAGCTCATTCAG 899
Db 10972 GGTGTGATCATGATGTGACTTCAACACCGTAAGTGTGGGCTCAGAGCTCATTCAG 11031
QY 900 TCGTCTGACCTCACTGCTTCAAAATCTGAATCAACTTCCCAATTGTGATGCCCTTGA 959
Db 11032 TCGTCTGACCTCACTGCTTCAAAATCTGAATCAACTTCCCAATTGTGATGCCCTTGA 11091
QY 960 GGAACATCCGATGACAAAGGCGCGCTCTTTCTCGGTGTACCTCCGAGCAAACTGC 1019
Db 11092 GGAACATCCGATGACAAAGGCGCGCTCTTTCTCGGTGTACCTCCGAGCAAACTGC 11151
QY 1020 GGTGTGTATGCCCTTACAGATGTAAGAACAGACAGCGGCTGTTCAGAGGCAAAAGAGA 1079
Db 11152 GGTGTGTATGCCCTTACAGATGTAAGAACAGACAGCGGCTGTTCAGAGGCAAAAGAGA 11211
QY 1080 ACTCAGAGAGCTGTGATCGTGAAGCAAGGCGCAAGCGCGAGGCTGTCTCAA 1139
Db 11212 ACTCAGAGAGCTGTGATCGTGAAGCAAGGCGCAAGCGCGAGGCTGTCTCAA 11271
QY 1140 GCGCCATGACTGGGAGGGGATCGTCTTTCCCAAGATGCCAGAGAGAGCATGATTA 1199
Db 11272 GCGCCATGACTGGGAGGGGATCGTCTTTCCCAAGATGCCAGAGAGAGCATGATTA 11331

QY 1200 GGTAGCTTGTGTGTAGCGCTCGAAAGAAATGACGCGGCTGTGTTTGTGTCTGC 1259
Db 11332 GGTAGCTTGTGTGTAGCGCTCGAAAGAAATGACGCGGCTGTGTTTGTGTCTGC 11391
QY 1260 ACTGAACCTTCTCTTATCTTGTGACATTCGCGGTTGTTTGTACTATTAATTAATT 1319
Db 11392 ACTGAACCTTCTCTTATCTTGTGACATTCGCGGTTGTTTGTACTATTAATTAATT 11451
QY 1320 GCCGCTGCTCAAGCTGAAATCC 1344
Db 11452 GCCGCTGCTCAAGCTGAAATCC 11476
RESULT 2
US-10-260-238-3410
Sequence 3410, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Kreps, Joel
APPLICANT: Provart, Nicholas
APPLICANT: Rieke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
PRIOR FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 3410
LENGTH: 1119
TYPE: DNA
ORGANISM: Trifolium aestivum
US-10-260-238-3410

Query Match 27.5%; Score 370; DB 15; Length 1119;
Best Local Similarity 100.0%; Pred. No. 3.8e-105; Indels 0; Gaps 0;
Matches 370; Conservative 0; Mismatches 0

QY 961 GAAACATCCGATGACAAAGCGCGCTCTTTCTCGGTGTACACTCCGAGAGAACTGCG 1020
Db 727 GAAACATCCGATGACAAAGCGCGCTCTTTCTCGGTGTACACTCCGAGAGAACTGCG 786
QY 1021 GTGTGTATGCCCTTACAGATGTAAGAACAGACAGCGGCTGTTCAGAGGCAAAAGAGA 1080
Db 787 GTGTGTATGCCCTTACAGATGTAAGAACAGACAGCGGCTGTTCAGAGGCAAAAGAGA 846
QY 1081 CTCAGAGAGCTGTGTGATGTGTAAGGAGGAGCAAGCGGCAACGCGGCAAGCTGTCCAAG 1140
Db 847 CTCAGAGAGCTGTGTGATGTGTAAGGAGGAGCAAGCGGCAACGCGGCAAGCTGTCCAAG 906
QY 1141 CGCCATGACTGGGAGGGGATCGTCTTTCCCAAGATGCCAGAGAGAGCATGATTAAG 1200
Db 907 CGCCATGACTGGGAGGGGATCGTCTTTCCCAAGATGCCAGAGAGAGCATGATTAAG 966
QY 1201 GTAGCTTGTGTGTAGCGCTCGAAAGAAATGACGCGGCTGTGTTGTGTGTGCTGCA 1260
Db 967 GTAGCTTGTGTGTAGCGCTCGAAAGAAATGACGCGGCTGTGTTGTGTGTGCTGCA 1026
QY 1261 CTGAACCTTCTCTTATCTTGTGACATTCGCGGTTGTTTGTACTATAATAATTG 1320
Db 1027 CTGAACCTTCTCTTATCTTGTGACATTCGCGGTTGTTTGTACTATAATAATTG 1086

QY 1321 CCCGTGGCGT 1330
1087 CCCGTGGCGT 1096

RESULT 3

US-10-434-893A-1
; Sequence 1, Application US/10434893A
; Publication No. US2004006083A1
; GENERAL INFORMATION:
; APPLICANT: Ahmed Regina
; APPLICANT: Matthew Kennedy Morell
; APPLICANT: Sadequr Rahman
; TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and star
; FILE REFERENCE: 69425
; CURRENT APPLICATION NUMBER: US/10/434,893A
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 1
; LENGTH: 2554
; TYPE: DNA
; ORGANISM: Hordeum vulgare
; FEATURE:
; OTHER INFORMATION: SSBELIA CDNA
US-10-434-893A-1

Query Match 19.6%; Score 263.6; DB 12; Length 2554;
Best Local Similarity 87.5%; Pred. No. 2.2e-71;
Matches 343; Conservative 0; Mismatches 24; Indels 25; Gaps 4;

QY 961 GAACATCCGCATGACACAGCGCGCTCTTTCTCGGTGTACACTCCGACAGAACTGCG 1020
DB 2128 GAACATCCGCATGACACAGCGCGCTCTTTCTCGGTGTACACTCCGACAGAACTGCG 2187
QY 1021 GTCGTGATGCCCTTACAGATGAAGAACACAGCGCGCTTTTTCACAGCAAGAGAGAA 1080
DB 2188 GTCGTGATGCCCTTACAGATGAAGAACACAGCGCGCTTTTTCACAGCAAGAGAGAA 2247
QY 1081 CTCGAGAGAGCTCGGTGATGCTGAGGAGACGACGCGGCAACGCGGAGCGCTCTCCAA 1140
DB 2248 CTCGAGAGAGCTCGGTGATGCTGAGGAGACGACGCGGCAACGCGGAGCGCTCTCCAA 2307
QY 1141 CGCCATGACTGGAGAGGATCGTGCCTCTTCCCAAGATCCAGAGAGAGAGATGATAG 1200
DB 2308 CGCCGATGATGGAGAGGATCGTGCCTCTTCCCAAGATCCAGAGAGAGATGATAG 2367
QY 1201 GTAGCTGTGGTGAAGCGCT-----CGAAGAAATGAGCGGCGCTGG 1243
DB 2368 GTAGCTGTGGTGAAGCGCTCGTTCATGAGTGAAGTGAAGAAATGAGCGGCGCTGG 2427
QY 1244 GTG-----TTGTGTGCTGCTGACGAAACCTCCCTCATCTGTGACATTCGCGGTGTTT 1299
DB 2428 GTGACATTTTGTAGTGTGCTGACGAAAC--CATCTATCTCTCAATTCGCGGTGTTT 2484
QY 1300 TGTACATAT-AACTATATATGCGCGTGGCGCT 1310
DB 2485 TGTACATATAACTAATATGCGCGTGGCGCT 2516

RESULT 4

US-09-792-127-1
; Sequence 1, Application US/09792127
; Patent No. US02002002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IId
; FILE REFERENCE: BBI439 US NA

; CURRENT APPLICATION NUMBER: US/09/792,127
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 2559
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-792-127-1

Query Match 9.1%; Score 122.6; DB 9; Length 2559;
Best Local Similarity 78.9%; Pred. No. 5.8e-27;
Matches 146; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGACACCAAGTATGTTTCAAGAAACATGAGAAAGATGATGATCATC 323
DB 1776 TTTATGACATCAAGCACCAAGTATGTTTCAAGAAACATGAGAAAGATGATGATCATC 1835
QY 324 CTCAAAAGAGAGATTTGTATTTTTCACCTTCCACTGAGCAATAGCTTTTTCAC 383
DB 1836 TTTGAAAAGAGAGCTTGTATTTTGTCAACTTCCACTGAGCAATAGCTTTTTCAC 1895
QY 384 TACCGTGTGGGTGTTCCAGCCTGGAGATGACAGATGATGCTTTTCATTGTCCA 443
DB 1896 TACCGGTGTGGGTGTTTAAAGCTTGGAGATGACAGATGATGCTTTTCATTGTCCA 1955
QY 444 CCCTT 448
DB 1956 CTCTT 1960

RESULT 5

US-09-792-127-3
; Sequence 3, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IId
; FILE REFERENCE: BBI439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-792-127-3

Query Match 9.1%; Score 122.6; DB 9; Length 3039;
Best Local Similarity 78.9%; Pred. No. 6.5e-27;
Matches 146; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGACACCAAGTATGTTTCAAGAAACATGAGAAAGATGATGATCATC 323
DB 2256 TTTATGACATCAAGCACCAAGTATGTTTCAAGAAACATGAGAAAGATGATGATCATC 2315
QY 324 CTCAAAAGAGAGATTTGTATTTTTCACCTTCCACTGAGCAATAGCTTTTTCAC 383
DB 2316 TTTGAAAAGAGAGCTTGTATTTTGTCAACTTCCACTGAGCAATAGCTTTTTCAC 2375
QY 384 TACCGTGTGGGTGTTCCAGCCTGGAGATGACAGATGATGCTTTTCATTGTCCA 443
DB 2376 TACCGGTGTGGGTGTTTAAAGCTTGGAGATGACAGATGATGCTTTTCATTGTCCA 2435
QY 444 CCCTT 448

Db 2436 CTCCTT 2440

RESULT 6

US-10-260-238-3480
Sequence 3480, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Kreps, Joel
APPLICANT: Provart, Nicholas
APPLICANT: Rieke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 3480
LENGTH: 1267
TYPE: DNA
ORGANISM: Triticum aestivum
US-10-260-238-3480

Query Match 9.1%; Score 122.4; DB 15; Length 1267;
Best Local Similarity 84.1%; Pred. No. 4.1e-27;
Matches 138; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 264 TTATGACATCTGAGCAGCATGATGTTCAACGAAACATGAGAAATAGGTATCATC 323
DB 513 TTATGACATCTGAGCAGCATGATGTTCAACGAAACATGAGAAATAGGTATCATC 572
QY 324 CTCGAAAGAGAGATTGTTGTTTTCACCTTCGAGCAATAGCTTTTGTGAC 383
DB 573 TTGAAAAAGGGAGCTTGATTTGTGTTCACTTCGAGAGTAGCTATTTCGAC 632
QY 384 TACCGGTGGGTGTTCCAGCCCTGGAGAGTACAGTAATCTT 427
DB 633 TACCGGTGGGTGTTTAAAGCTGGAGAGTACAGTAATCTT 676

RESULT 7

US-10-260-238-5563
Sequence 5563, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Kreps, Joel
APPLICANT: Provart, Nicholas
APPLICANT: Rieke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238

CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 5563
LENGTH: 636
TYPE: DNA
ORGANISM: Zea mays
US-10-260-238-5563

Query Match 9.0%; Score 120.6; DB 15; Length 636;
Best Local Similarity 82.6%; Pred. No. 9.2e-27;
Matches 138; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 262 AGTTATGACATCTGAGCAGCATGATGTTCAACGAAACATGAGAAATAGGTATCA 321
DB 323 AATTCATGACATCTGATCAGCAGTADATTTCGGAACATGAGAGATTAAGTATTC 382
QY 322 TCCTCAAAAGAGAGATTGTTGTTTTCACCTTCACCTGAGCAATAGCTTTTTC 381
DB 383 TGTTGAAAAAGGAGATTGTTGTTTTCACCTTCACCTGCAACACAGCTATTTC 442
QY 382 ACTACCGTTGGGTGTTCCAGCCTGGAGAGTACAGGTATGCTTG 428
DB 443 ACTACCGTTGGGTGTTTCGAAAGCTGGGTGTTATAGGTGCTTG 489

RESULT 8

US-10-434-893A-2
Sequence 2, Application US/10434893A
Publication No. US2004006083A1
GENERAL INFORMATION:
APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morell
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and suc
TITLE OF INVENTION: containing products with an increased amylose content
FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 2.1
SEQ ID NO 2
LENGTH: 2780
TYPE: DNA
ORGANISM: Hordeum vulgare
FEATURE:
OTHER INFORMATION: SSBEIIB cDNA
US-10-434-893A-2

Query Match 8.9%; Score 119.6; DB 12; Length 2780;
Best Local Similarity 84.8%; Pred. No. 5.4e-26;
Matches 134; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 264 TTATGACATCTGAGCAGCATGATGTTTCACGAAACATGAGAAATAGGTATCATC 323
DB 2182 TTATGACATCTGAGCAGCATGATGTTTCGAAACATGAGAAATAGGTATCATC 2241
QY 324 CTCGAAAGAGAGATTGTTGTTTTCACCTTCGAGCAATAGCTTTTGTGAC 383
DB 2242 TTGAAAAAGGGAGCTTGATTTGTGTTCACTTCGAGAGTAGCTATTTCGAC 2301
QY 384 TACCGGTGGGTGTTCCAGCCCTGGAGAGTACAGGT 421
DB 2302 TACCGGTGGGTGTTTAAAGCTGGAGAGTACAGGT 2339

RESULT 9

US-10-260-238-1027

```
/ Sequence 1027, Application US/10260238
/ Publication No. US20040016025A1
/ GENERAL INFORMATION:
/ APPLICANT: Budworth, Paul R.
/ APPLICANT: Moughamer, Todd G.
/ APPLICANT: Briggs, Steven P.
/ APPLICANT: Cooper, Bret
/ APPLICANT: Glazebrook, Jane
/ APPLICANT: Goff, Stephen A.
/ APPLICANT: Katagiri, Fumiyaki
/ APPLICANT: Kieps, Joel
/ APPLICANT: Provart, Nicholas
/ APPLICANT: Rieke, Darrell
/ APPLICANT: Zhu, Tong
/ TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
/ FILE REFERENCE: 60111-NP
/ CURRENT APPLICATION NUMBER: US/10/260,238
/ CURRENT FILING DATE: 2002-09-26
/ PRIOR APPLICATION NUMBER: US 60/325,448
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: US 60/325,277
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: US 60/370,620
/ PRIOR FILING DATE: 2002-04-04
/ NUMBER OF SEQ ID NOS: 6077
/ SEQ ID NO 1027
/ LENGTH: 1642
/ TYPE: DNA
/ ORGANISM: Oryza sativa
US-10-260-238-1027

Query Match      8.0%; Score 107.2; DB 15; Length 1642;
Best Local Similarity 77.4%; Pred. No. 3e-22;
Matches 130; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 259 TGCAGTTTATGACATCTTGAGCACCAGTATGTTTCACGGAACATGAGAAATAGGTGA 318
DB 1281 TGGGGTTCATGACATCAGACACCAGTACATCTCGAAAGCATGAAAGATGAATGA 1340
QY 319 TCATCCTCAAAAGAGAGATTGGTATTTGTTTCACTTCACCTGAGCAATAGCTTT 378
DB 1341 TTATATTTGAAAGAGAGATCTGGTATTTGTTCAACTTCATGAGATTAACGCTATT 1400
QY 379 TTGACTACCGTGTGGGTGTTCCAGCCTGGGAAGTAAAGGTATGCT 426
DB 1401 TTGACTACCGTGTGGGTGTTTAAAGCCAGGAAATATTAAGAGTGGT 1448

RESULT 10
US-09-770-149-955/C
/ Sequence 955, Application US/09770149
/ Patent No. US20020059663A1
/ GENERAL INFORMATION:
/ APPLICANT: Gorlach, Jorn
/ APPLICANT: An, Yong-Qiang
/ APPLICANT: Hamilton, Carol M.
/ APPLICANT: Price, Jennifer L.
/ APPLICANT: Raines, Tracy M.
/ APPLICANT: Yu, Yang
/ APPLICANT: Rameaka, Joshua G.
/ APPLICANT: Page, Amy
/ APPLICANT: Matthew, Abraham V.
/ APPLICANT: Ledford, Brooke L.
/ APPLICANT: Woessner, Jeffrey P.
/ APPLICANT: Haas, William David
/ APPLICANT: Garcia, Carlos A.
/ APPLICANT: Kricker, Maja
/ APPLICANT: Slader, Ted
/ APPLICANT: Davis, Keith R.
/ APPLICANT: Allen, Keith
/ APPLICANT: Hoffman, Neil
/ APPLICANT: Hurban, Patrick
/ TITLE OF INVENTION: Expressed Sequences of Arabidopsis
```

```
/ TITLE OF INVENTION: thaliana
/ FILE REFERENCE: 2024 (PAPA-013PRV)
/ CURRENT APPLICATION NUMBER: US/09/770,149
/ CURRENT FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/178,506
/ PRIOR FILING DATE: 2000-01-27
/ NUMBER OF SEQ ID NOS: 999
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 955
/ LENGTH: 602
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-09-770-149-955

Query Match      7.2%; Score 97; DB 9; Length 602;
Best Local Similarity 70.3%; Pred. No. 2.4e-19;
Matches 130; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGCACCAGTATGTTTCACGGAACATGAGAAATAGGTATCATC 323
DB 490 TTTATGACTTCGAGCACCAGTATCATATCAAGAAAGCAGAGAGATAGATATCGTA 431
QY 324 CTCAAAAGAGAGATTGGTATTTGTTTCACTTCACCTGAGCAATAGCTTTTTCAC 383
DB 430 TTGAAAAGAGGTATCTCGTCTTGTCTTTAACTTCACTGACGACGACTACTTGAT 371
QY 384 TACCGTGTGGTGTTCACAGCCTGGAGAGTACAGATGATGCTTTTCATTGTCGA 443
DB 370 TACCGCATTTGTTGCTTCACAGCCTGGAAATATATAGATCGATTGAGACTCGAGCATCT 311
QY 444 CCCTT 448
DB 310 CTCCT 306

RESULT 11
US-09-938-842A-872
/ Sequence 872, Application US/09938842A
/ Patent No. US20020160378A1
/ GENERAL INFORMATION:
/ APPLICANT: Harper, Jeff
/ APPLICANT: Kieps, Joel
/ APPLICANT: Wang, Xun
/ APPLICANT: Zhu, Tong
/ TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
/ TITLE OF INVENTION: SAME, AND METHODS OF USE
/ FILE REFERENCE: SCDP1300-3
/ CURRENT APPLICATION NUMBER: US/09/938,842A
/ CURRENT FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: US 60/227,866
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: US 60/264,647
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/300,111
/ PRIOR FILING DATE: 2001-06-22
/ NUMBER OF SEQ ID NOS: 5379
/ SEQ ID NO 872
/ LENGTH: 2418
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-09-938-842A-872

Query Match      7.2%; Score 97; DB 9; Length 2418;
Best Local Similarity 70.3%; Pred. No. 6.4e-19;
Matches 130; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGCACCAGTATGTTTCACGGAACATGAGAAATAGGTATCATC 323
DB 2098 TTTATGACTTCGAGCACCAGTATCATATCAAGAAAGCAGAGAGATAGATATCGTA 2157
QY 324 CTCAAAAGAGAGATTGGTATTTGTTTCACTTCACCTGAGCAATAGCTTTTTCAC 383
DB 2158 TTGAAAAGAGGTATCTCGTCTTGTCTTTAACTTCACTGACGACGACTACTTGAT 2217
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QY 384 TACCGTGTGGTGTTCACAGCCCTGGAGATACAGGATGATGCTTTCATTGTCGA 443
Db 2218 TACCGCATTTGTTGCTCTCCAGCTGGAAATATATAGATGATGACTCGGAGATCTT 2277
QY 444 CCCTT 448
Db 2278 CTCTT 2282

RESULT 12
US-09-938-842A-872
Sequence 872, Application US/09338842A
Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Krepes, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 872
LENGTH: 2418
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-872

Query Match 7.2%; Score 97; DB 11; Length 2418;
Best Local Similarity 70.3%; Pred. No. 6.4e-19;
Matches 130; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 264 TTATGATCATGTGACACCAAGTATGTTTCACGAAACATGAGAGATAGGTGATCATC 323
Db 2098 TTATGATCTTCGAGACCAATTCATATCAGAAAAGAGAGAGATAGATATCGTA 2157
QY 324 CTCAAAAGAGAGATTGGTATTTGTTTTCACCTTCAGTGAAGAAATAGCTTTTTCAC 383
Db 2158 TTCGAAAGAGGTGATCTGCTCTTTGCTTTTAACTTCAGTGAAGAGAGCTTCTTGTAT 2217
QY 384 TACCGTGTGGTGTTCACAGCCCTGGAGATACAGGATGATGCTTTCATTGTCGA 443
Db 2218 TACCGCATTTGTTGCTCTCCAGCTGGAAATATATAGATGATGACTCGGAGATCTT 2277
QY 444 CCCTT 448
Db 2278 CTCTT 2282

RESULT 13
US-10-056-454A-17
Sequence 17, Application US/10056454A
Publication No. US20030166919A1
GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Unidigma Blvd.
CITY: Newcasttle
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-056-454A-17

Query Match 7.1%; Score 95.4; DB 14; Length 2529;
Best Local Similarity 69.0%; Pred. No. 2.1e-18;
Matches 129; Conservative 1; Mismatches 57; Indels 0; Gaps 0;
QY 262 AGTTATGATCATGTGACACCAAGTATGTTTCACGAAACATGAGAGATAGGTGATCA 321
Db 2175 AGTTATGATCTTCAGAACCACTTATCATATCAGAAAGATGAGAGATAGATGTTG 2234
QY 322 TCCTCAAAAGAGAGATTGGTATTTGTTTTCACCTTCAGTGAAGAAATAGCTTTTTCG 381
Db 2235 TATTGAAAFAGAGAACTAGATTTTGTCTTTTATTTTCAGTGAAGAAATAGCTATTCAG 2294
QY 382 ACTACCGTGTGGTGTTCACAGCCCTGGAGATACAGGATGATGCTTTCATTGTC 441
Db 2295 ACTATGCAATAGGCTGCTGAAGCTGGAAATATCAAGGTGCTTGACTGACTGATGATC 2354
QY 442 CACCTT 448
Db 2355 CACTTTT 2361

RESULT 14
US-10-056-454A-13
Sequence 13, Application US/10056454A
Publication No. US20030166919A1
GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Unidigma Blvd.
CITY: Newcasttle
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-056-454A-13

Query Match 6.9%; Score 92.6; DB 14; Length 2975;
Best Local Similarity 68.4%; Pred. No. 1.8e-17;
Matches 128; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 03:15:20 ; Search time 3546.4 Seconds
(without alignments)
11317.033 Million cell updates/sec

Title: US-09-508-377-10_COPY_10120_11463

Sequence: 1 ttgatatcgtgtatgcaaa.....tcgcctcaacgtgaatacc 1344

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST.*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estrov:*
6: em_estropl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_estfun:*
15: em_estrom:*
16: em_estrom:*
17: em_gse_hum:*
18: em_gse_inv:*
19: em_gse_pin:*
20: em_gse_vrt:*
21: em_gse_fun:*
22: em_gse_mam:*
23: em_gse_mus:*
24: em_gse_pro:*
25: em_gse_rod:*
26: em_gse_phg:*
27: em_gse_vrl:*
28: gb_gsal:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	464.8	34.6	724	13	BU607192	IG7 wheat
2	370	27.5	610	14	CD912768	G550.115M
3	366.8	27.3	573	13	BQ237446	TAR05016F
4	365.8	27.2	1107	14	CK210642	FGAS02246

5	361.6	26.9	447	9	AJ604482	AJ604482
6	361.6	26.9	622	14	CD890410	CD890410 G118.114T
7	360.4	26.8	405	13	BQ242270	TAE15032A
8	359.6	26.8	692	14	CD895041	CD895041 G118.127M
9	358.4	26.7	414	12	BJ270799	BJ270799
10	358.4	26.7	491	12	BJ232268	BJ232268
11	358.4	26.7	897	14	CK153053	CK153053 FGAS03160
12	358.4	26.7	721	12	BJ273375	BJ273375
13	358.4	26.3	527	14	CD934119	CD934119 GR45.123A
14	347.6	25.9	532	14	CD899313	CD899313 G174.110D
15	347.6	25.9	565	14	CD897227	CD897227 G174.105D
16	347.6	25.9	569	12	BJ267927	BJ267927
17	347.6	25.9	680	14	CD901305	CD901305 G356.103G
18	347.6	25.9	749	14	CD899779	CD899779 G174.113I
19	345	25.7	350	6	AL810271	AL810271 Triticum
20	343.6	25.6	470	12	BQ237912	BQ237912
21	341.4	25.4	556	13	BQ238322	BQ238322 TAE05005F
22	339.6	25.3	593	14	CD929440	CD929440 GR45.108C
23	338.6	25.0	651	14	CD453536	CD453536 WHE0803.A
24	335	24.9	484	13	BQ237604	BQ237604
25	331	24.6	450	12	BM137874	WHE0472.E
26	331	24.6	537	13	BQ276381	BQ276381
27	330	24.6	383	12	BQ579812	BQ579812 WHE2974.G
28	319.6	23.8	339	12	BJ275791	BJ275791
29	319	23.7	554	14	CA637960	CA637960 wheat.pko
30	310	23.1	744	14	CD929759	CD929759 GR45.109A
31	308	22.9	341	14	CA739027	CA739027 wpl28.pko
32	293.6	21.8	358	13	BQ282638	BQ282638 WHE3074.H
33	283.4	21.1	334	12	BJ272536	BJ272536
34	280.4	20.9	354	12	BJ267589	BJ267589
35	277	20.6	456	12	BJ466312	BJ466312
36	263.6	19.6	479	12	BJ464040	BJ464040
37	263.6	19.6	547	9	AV919407	AV919407 AV919407
38	263.6	19.6	572	14	CB875153	CB875153 HX07403W
39	263.6	19.6	629	13	BQ471544	BQ471544 HV0202L24R
40	263.6	19.6	628	9	AJ432603	AJ432603 AJ432603
41	263.6	19.6	766	12	BT948391	BT948391 HYVME1000
42	262	19.5	586	14	CB871991	CB871991 HC06B22Y
43	256.6	19.1	642	10	AW982619	AW982619 HVSME9000
44	255.8	19.0	688	9	AV944141	AV944141 AV944141
45	255.6	19.0	607	12	BJ482532	BJ482532

ALIGNMENTS

RESULT 1	BU607192	724 bp	mRNA	linear	EST 23-SEP-2002
LOCUS	IG7 wheat	seed cDNA library	Triticum aestivum	cDNA, mRNA	sequence.
DEFINITION	BU607192				
ACCESSION	BU607192.1	GI:23270467			
VERSION					
KEYWORDS	EST.				
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Triticum aestivum				
REFERENCE	Li, J., Wang, F., Li, Q., and Zhang, X.				
AUTHORS	1 (bases 1 to 724)				
TITLE	Expressed sequence tags analysis of a wheat seed cDNA library				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Xiansheng Zhang				
	Plant development molecular biology lab				
	college of life sciences				
	Shan dong agriculture university, Tai'an, Shan dong, China				
	Tel: 086-0538-8241144				
	Email: zhiwu@sdau.edu.cn.				
FEATURES	Location/Qualifiers				
source	1..724				
	/organism="Triticum aestivum"				
	/mol_type="mRNA"				
	/db_xref="taxon:4565"				

ORIGIN

/cissue_type="seed"
/clone_lib="wheat seed cDNA library"

Query Match 34.6%; Score 464.8; DB 13; Length 724;
Best Local Similarity 81.1%; Pred. No. 1.5e-125;
Matches 618; Conservative 0; Mismatches 52; Indels 92; Gaps 3;

581 AGAAGAGTTTCTTCAACAGCCCGGAAAGCATATCCATCTTCAATATATCTACTTAAG 640
24 AGGTTCACCGTATCGATAGCTTATATCGAATTCGCGGATTCATATATATCTACTTAAG 83
641 TGTGTTGTTAACTTATGCTGAGTGAATCGGATCGATATACAGATCTATTTCCGAA 700
84 GGTGTTTCAATCTTGTACTGATGAGCTCACTCTTAATCTGAACTGTTTACCGAA 143
701 TCTACCTTAACCATCTTACAGAGTTTAAAGCAGCCCATTTGACAAATTTGGCTGGTTT 760
144 TCTACCTTAACCATCTTACAGAGTTTAAAGCAGCCCATTTGACAGTCCACTGGGTTTA 203
761 TGTGTTGTTAACTTATGCTGAGTGAATCGGATCGATATACAGATCTTGAAGATGA 820
204 GTTGTGTTGAGCAGTTTCTGCTATTTCTT-ATCAGGTGGCTTAACTCCAGCATGCA 262
821 CTCTTTGTTGAGATCAGAGGCTTATGATGATGATGATGATGATGATGATGATGATG 880
263 CTCTTTGTTGAGATCAGAGGCTTATGATGATGATGATGATGATGATGATGATGATG 313
881 GGGTCAAGCGCTCACTGCTGCTTGAATCACTGCTTGAATCACTGATCACTTCC 940
314 ----- 313
941 AATTGCTGATGCCCTTGAGAGAAATCCGATGACAAAGCGCGCTCTTTCTGGTGT 1000
314 -----GAAACATCCGATGACAAAGCGCGCTCTTTCTGGTGT 353
1001 AACTCCGAGAGAACTGCGGTGATGAGCTTACAGAGTAAAGACAGAGCGGCTT 1060
354 AACTCCGAGAGAACTGCGGTGATGAGCTTACAGAGTAAAGACAGAGCGGCTT 413
1061 GTTACAAAGCGAGAGAGAACTCCAGAGAGCTGATGATGATGATGATGATGATGATG 1120
414 GTTACAAAGCGAGAGAGAACTCCAGAGAGCTGATGATGATGATGATGATGATGATG 473
1121 CGGCGCGAGAGCTGCTCCAAAGGCGCTGATGATGATGATGATGATGATGATGATG 1180
474 CGGCGCGAGAGCTGCTCCAAAGGCGCTGATGATGATGATGATGATGATGATGATG 533
1181 CAG 1240
534 CAG 593
1241 TGGGTGTTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1300
594 TGGGTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651
1301 GTACAT 1342
652 GTACAT 693

RESULT 2
CD912768/c CD912768 610 bp mRNA linear EST 14-VTL-2003
LOCUS G550.115M08R010903 G550 Triticum aestivum cDNA clone G550.115M08,
DEFINITION mRNA sequence.
ACCESSION CD912768
VERSION CD912768.1 GI:32687092
KEYWORDS EST,
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE

Poideae; Triticaceae; Triticum.
1 (bases 1 to 610)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).

FEATURES

source

1..610
/organism="Triticum aestivum"

/mol_type="mRNA"

/culivar="rectal"

/db_xref="taxon:4565"

/clone="G550115M08"

/cissue_type="grain (550 degrees per day after
pollination)"

/clone_lib="G550"

ORIGIN

Query Match 27.5%; Score 370; DB 14; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.4e-97;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

961 GAACATCCGATGACAAAGAGCGCGCTCTTCTGCTGATCACTCCGAGCAACTGCG 1020
421 GAACATCCGATGACAAAGAGCGCGCTCTTCTGCTGATCACTCCGAGCAACTGCG 362
1021 GTGCTGATGCCCTTACAGATGAAGAACAGAGCGGCTGTTACAGAGCAAGAGAA 1080
361 GTGCTGATGCCCTTACAGATGAAGAACAGAGCGGCTGTTACAGAGCAAGAGAA 302
1081 CTCAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
301 CTCAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 242
1141 CGGCATGACTGGAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATG 1200
241 CGGCATGACTGGAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATG 182
1201 GTAGCTTGTGTGAGAGGCTCGAAAGAAATGAGAGGCGCTGGGTGTTGTGCTGCA 1260
181 GTAGCTTGTGTGAGAGGCTCGAAAGAAATGAGAGGCGCTGGGTGTTGTGCTGCA 122
1261 CTGACCCCTCTCTATCTTCAATATCCGAGTTGTTTGTACATATATATATATAT 1320
121 CTGACCCCTCTCTATCTTCAATATCCGAGTTGTTTGTACATATATATATATAT 62
1321 CCCGTGGCT 1330
61 CCCGTGGCT 52

RESULT 3

BQ237446/c BQ237446 573 bp mRNA linear EST 03-MAY-2002
LOCUS TA05016F12F TA05 Triticum aestivum cDNA clone TA05016F12F, mRNA
DEFINITION sequence.
ACCESSION BQ237446
VERSION BQ237446.1 GI:20433322
KEYWORDS EST,
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Poideae; Triticaceae; Triticum.
REFERENCE 1 (bases 1 to 573)
Cloutier,S.

TITLE
JOURNAL
COMMENT
Wheat functional genomics - Glenlea developing seeds cDNA libraries
Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Datoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@agr.gc.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 016 row: F column: 12
Seq primer: M13 Forward.
Location/Qualifiers
1. 573
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone="TAE05016F12F"
/tissue_type="developing seeds"
/dev_stage="5 days after anthesis"
/lab_host="E. coli DH10B"
/clone_lib="TAE05"
/note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
NotI; Site_2: MluI; mRNA obtained from wheat seeds of
cultivar Glenlea 5 days post-anthesis"

ORIGIN

Query Match 27.3%; Score 366.8; DB 13; Length 573;
Best Local Similarity 99.5%; Pred. No. 1.2e-96;
Matches 368; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 961 GAACATCCGATGACACACAGGCGGCTTTCTCGGTGTAACCTCCGACGAATCGG 1020
DB 413 GAACATCCGATGACACACAGGCGGCTTTCTCGGTGTAACCTCCGACGAATCGG 354
QY 1021 GTCGTGATGCCCTTACAGAGTAAGAACAGGAGGCTTTTACAGGCAAGAGAGAA 1080
DB 353 GTCGTGATGCCCTTACAGAGTAAGAACAGGAGGCTTTTACAGGCAAGAGAGAA 294
QY 1081 CTCAGAGAGCTCGTGAATCGTGAAGCAAGAGGCAAGGCGGAGGCTGCTCCAA 1140
DB 293 CTCAGAGAGCTCGTGAATCGTGAAGCAAGAGGCAAGGCGGAGGCTGCTCCAA 234
QY 1141 CGCCATGACTGGAGGAGGATCGTGCCTCTTCCCAAGATCCAGAGAGAGATGATG 1200
DB 233 CGCCATGACTGGAGGAGGATCGTGCCTCTTCCCAAGATCCAGAGAGAGATGATG 174
QY 1201 GTACTTGTGGTGAGCCCTCGAAGAAATGAGAGGCGGCTGGGTGTTGTGTGCTGA 1260
DB 173 GTAGCTTGTGGTGAGCCCTCGAAGAAATGAGAGGCGGCTGGGTGTTGTGTGCTGA 114
QY 1261 CTGAACCTCTCCCTATCTTGACATTCGCCGTTGTTTGTATATATAATATTG 1320
DB 113 CTGAACCTCTCCCTATCTTGACATTCGCCGTTGTTTGTATATATAATATTG 54
QY 1321 CCCGTGCGCT 1330
DB 53 CCCGTGCGCT 44

RESULT 4
LOCUS CK210642 1107 bp mRNA linear EST 08-DEC-2003
DEFINITION FGAS022466 Triticum aestivum FGAS: Library 5 GATE 7 Triticum
aestivum cDNA, mRNA sequence.
ACCESSION CK210642
VERSION CK210642.1 GI:39573032
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 1107)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Lemke, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress in Wheat and Canola Crops
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas.estres@usask.ca

FEATURES
source
1. 1107
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"
/note="Vector: pCMV.SPORT6; Crown and developmental stages
of spike formation in wheat cultivar Norstar. 4 mRNA
populations were combined before constructing the library.
The first mRNA population is from 1cm crown sections after
30 days of cold acclimation. The second is from 1cm crown
sections after 11 days of deacclimation (before
deacclimation plants were fully vernalized for 49 days).
The third is from different developmental stages of spike
formation (5 to 50mm) that still have not emerged from the
leaf (dissection required). The last is from different
developmental stages of spike and seed formation after
having emerged from the leaf (visible). First strand
synthesis in this library was done in the presence of
methylated dCTP thereby protecting from internal cleavage
with NotI."

ORIGIN

Query Match 27.2%; Score 365.8; DB 14; Length 1107;
Best Local Similarity 99.2%; Pred. No. 3e-96;
Matches 367; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 961 GAACATCCGATGACACACAGGCGGCTTTCTCGGTGTAACCTCCGACGAATCGG 1020
DB 477 GAACATCCGATGACACACAGGCGGCTTTCTCGGTGTAACCTCCGACGAATCGG 536
QY 1021 GTCGTGATGCCCTTACAGAGTAAGAACAGGAGGCTTTTACAGGCAAGAGAGAA 1080
DB 537 GTCGTGATGCCCTTACAGAGTAAGAACAGGAGGCTTTTACAGGCAAGAGAGAA 596
QY 1081 CTCAGAGAGCTCGTGAATCGTGAAGCAAGAGGCAAGGCGGAGGCTGCTCCAA 1140
DB 597 CTCAGAGAGCTCGTGAATCGTGAAGCAAGAGGCAAGGCGGAGGCTGCTCCAA 656
QY 1141 CGCCATGACTGGAGGAGGATCGTGCCTCTTCCCAAGATCCAGAGAGAGATGATG 1200
DB 657 CGCCATGACTGGAGGAGGATCGTGCCTCTTCCCAAGATCCAGAGAGAGATGATG 716
QY 1201 GTAGCTTGTGGTGAGCCCTCGAAGAAATGAGAGGCGGCTGGGTGTTGTGTGCTGA 1260
DB 717 GTAGCTTGTGGTGAGCCCTCGAAGAAATGAGAGGCGGCTGGGTGTTGTGTGCTGA 776
QY 1261 CTGAACCTCTCTATCTTGACATTCGCCGTTGTTTGTATATATAATATTG 1320
DB 777 CTGAACCTCTCTATCTTGACATTCGCCGTTGTTTGTATATATAATATTG 836

Qy	1321	CCCCGCGCT	1330
Db	837	CCCGTCCGCT	846

RESULT 5					
AJ604482					
LOCUS					
DEFINITION					
	AJ604482	447 bp	mrna	linear	EST 03-NOV-2003
	AJ604482 T07	Triticum	aestivum	clone H12_T07_plate_9,	mrna
	sequence.				

ORGANISM	Triticum aestivum (bread wheat)
SOURCE	Triticum aestivum
KEYWORDS	
VERSION	EST.
ACCESSION	AF604482.1
GI	3153674

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 447)	Zhang,D., Klieva,N., Barker,G.L.A., Wilson,I.D., Edwards,K.J., Close,T.J., Zheng,H., McCattor,K., Soares,B.M. and Nguyen,H.T.	Combining expressed-sequence-tags sequencing and subtractive hybridization for rapid identification of differentially expressed genes under heat stress in wheat (<i>Triticum aestivum</i> (L.) Moench)	Unpublished (2002)	
Contact:	Barker GL			
	Biological Sciences			
	University of Bristol			
	Woodland Road Bristol, BS8 1UG, United Kingdom.			

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FEATURES
source
Location/Qualifiers
1. .447
/Source: "ITC-Edison Technology"

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/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Mustang"
/db_xref="taxon:4565"
/clone="H12 T07 plate_9"
/tissue_type="Heat stressed whole seedlings"
/dev_stage="2 weeks old"
/clone_lib="T07"

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Query Match	26.9%	Score 361.6	DB 9	Length 447
Best Local Similarity	98.4%	Pred. No. 3,7e-95		
Matches 376	Conservative 0	Mismatches 4	Indels 2	Gaps 1

QY	961	AAACATCCGATGACAAACAGGCGGGCTCTTCTCGGTACACTCCAGACGAACCTCG	102
Db	63	GAACATCCGATGACAAACAGGCGGGCTCTTCTCGGTACACTCCAGACGAACCTCG	122
QY	1021	GTCTGTATGCGCTTACAGAGTAAGAACACAGCGGCTTGTATTACAGGCCAAAGAGAA	1098
Db	123	GTCTGTATGCGCTTACAGAGTAAGAACACAGCGGCTTGTATTACAGGCCAAAGAGAA	182
QY	1081	CTCCAGAGAGCTCTGTGATCTGTAGACGAAAGCGACGGGCGAACGGCGCGGAGGCTGCTCAAG	1144
Db	183	CTCCAGAGAGCTCTGTGATCTGTAGACGAAAGCGACGGGCGAACGGGCTGCTCAAG	242
QY	1141	CGCCATGACTGGGAGGGAGTGGTGCTCTTCCCGAGATGCCAGAGAGACAGATGGATAG	1200
Db	243	CGCCATGACTGGGAGGGAGTGGTGCTCTTCCCGAGATGCCAGAGAGACAGATGGATAG	302
QY	1201	GTAGCTTGTGGTGAAGCGCTCGAAAGAAATGAGCGGGCTGGGTGTTGTGTGCTGCA	1266
Db	303	GTAGCTTGTGGTGAAGCGCTCGAAAGAAATGAGCGGGCTGGGTGTTGTGTGCTGCA	362
QY	1261	CTGAACCTCTCTCTATCTTTGACACATTCGCCGTTGTTTTGTACATATACTAATATTG	1322
Db	363	CT--ACCTCTCTCTATCTTTGACACATTCGCCGTTGTTTTGTACATATACTAATATTG	420
QY	1321	CCCGTGGCGTCAACGTGAATAAT	1342
Db	421	CCGTGGCGTCAACGTGAACAT	442

RESULT 6	CD890410/c	LOCUS	DEFINITION
CD890410	622 bp	mRNA	linear
G118.114J06R010926	G118	Triticum aestivum	EST 14-JUL-2003
mRNA sequence.			
cdna clone G118114J06,			

ACCESSION	CD890410
VERSION	CD890410.1
KEYWORDS	GI:32659747
SOURCE	E87.
ORGANISM	Triticum aestivum (bread wheat)
	Triticum aestivum
	Triticum aestivum
	Mitochondrial DNA; Strontophyta; Embryophyta; Tracheophyta;

REFERENCE	1 (bases 1 to 622)
AUTHORS	Genoplane.
TITLE	Genoplane, a major partnership french program in plant genomics
JOURNAL	Unpublished (2003)
COMMENT	Contact: Genoplane Genoplane

Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiosgen.fr>).

FEATURES	Location/Qualifiers
source	1. .622

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/organism="Triticum aestivum"
/mol_type="mRNA"
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pollination)"
/clone_lib="G118"

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Query March	26.9%	Score 361.6	DB 14	Length 622
Best Local	98.4%	Prod. No. 4.2e-95		
Matches 376	Conservative	0	Mismatches 4	Indels 2
				Gaps 1

[illegible]

BQ242270/c 405 bp mRNA linear EST 03-MAY-2002
LOCUS TA815032A02F Ta815 Triticum aestivum CDNA clone TA815032A02F, mRNA
DEFINITION sequence.
ACCESSION BQ242270.1 GI:20438146
VERSION BQ242270.1
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 405)
Cloutier, S.
REFERENCE Wheat functional genomics - Glenlea developing seeds cDNA libraries
JOURNAL Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereals Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@agr.gc.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >1.4 kb
Plate: 032 row: A column: 02
Seq primer: M13 Forward.
location/Qualifiers
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/cultivar="Glenlea"
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/clone="TA815032A02F"
/tissue_type="developing seeds"
/dev_stage="15 days after anthesis"
/lab_host="E. coli DH10B"
/clone_id="TA815"
/note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies);
Site 1: NciI; Site 2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea 15 days post-anthesis"

Query Match 26.8%; Score 360.4; DB 13; Length 405;
Best Local Similarity 98.4%; Pred. No. 8.1e-95;
Matches 364; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

961 GAACATCCGCATGACACAGCGCGGCTTTCTCGGTGACACTCCGACGAACTGCG 1020
DB GAAATCCGCATGACACAGCGCGGCTTTCTCGGTGACACTCCGACGAACTGCG 335
1021 GTGCGTATGCCCTTACAGAGTAAGAACACAGAGCGGCTTTTACAGGCAAGAGAGAA 1080
DB GTGCGTATGCCCTTACAGAGTAAGAACACAGAGCGGCTTTTACAGGCAAGAGAGAA 275
334 GTGCGTATGCCCTTACAGAGTAAGAACACAGAGCGGCTTTTACAGGCAAGAGAGAA 275
1081 CTCAGAGAGCTCTGTATCTGTAGCGAAGCAAGCGGCAAGCGGCGAGGCTGCTCAAG 1140
DB CTCAGAGAGCTCTGTATCTGTAGCGAAGCAAGCGGCAAGCGGCGAGGCTGCTCAAG 215
274 CTCAGAGAGCTCTGTATCTGTAGCGAAGCAAGCGGCGAGGCTGCTCAAG 215
1141 CGCCATGACTGGGAGGGGATGCTGCTCTTCCCAATATGCCAGAGAGAGATGATAG 1200
DB CGCCATGACTGGGAGGGGATGCTGCTCTTCCCAATATGCCAGAGAGAGATGATAG 155
214 CGCCATGACTGGGAGGGGATGCTGCTCTTCCCAATATGCCAGAGAGAGATGATAG 155
1201 GTAGCTTGTGTAGCGCTCGAAGAAATGAGACGGGCTGGGCTTTGTTGTGCTGCA 1260
DB GTAGCTTGTGTAGCGCTCGAAGAAATGAGACGGGCTGGGCTTTGTTGTGCTGCA 95
154 GTAGCTTGTGTAGCGCTCGAAGAAATGAGACGGGCTGGGCTTTGTTGTGCTGCA 95
1261 CTGAACCTCTCTCTATCTTGACATCTCCGGTGTGTTTGTACATATAATTAATTG 1320
DB CTGAACCTCTCTCTATCTTGACATCTCCGGTGTGTTTGTACATATAATTAATTG 35
94 CTGAACCTCTCTCTATCTTGACATCTCCGGTGTGTTTGTACATATAATTAATTG 35
1321 CCGGTGGCT 1330
|||||

DB 34 CCGGTGGCTT 25
RESULT 8
CD895041
LOCUS G118.127M24F010824 G118 Triticum aestivum CDNA clone G118127M24,
DEFINITION mRNA sequence.
ACCESSION CD895041 GI:32667199
VERSION CD895041
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 692)
Genoplatne.
REFERENCE Genoplatne, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
Contact: Genoplatne
Genoplatne
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>
and <http://genoplatne-info.infobiogen.fr>).
location/Qualifiers
FEATURES
source
1..692
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/cultivar="rectal"
/db_xref="taxon:4565"
/clone="G118127M24"
/tissue_type="grain (118 degrees per day after
pollination)"
/clone_id="G118"

Query Match 26.8%; Score 359.6; DB 14; Length 692;
Best Local Similarity 97.9%; Pred. No. 1.7e-94;
Matches 374; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

961 GAACATCCGCATGACACAGCGCGGCTTTCTCGGTGACACTCCGACGAACTGCG 1020
DB GAAATCCGCATGACACAGCGCGGCTTTCTCGGTGACACTCCGACGAACTGCG 350
291 GAACATCCGCATGACACAGCGCGGCTTTCTCGGTGACACTCCGACGAACTGCG 350
1021 GTGCGTATGCCCTTACAGAGTAAGAACACAGAGCGGCTTTTACAGGCAAGAGAGAA 1080
DB GTGCGTATGCCCTTACAGAGTAAGAACACAGAGCGGCTTTTACAGGCAAGAGAGAA 410
351 GTGCGTATGCCCTTACAGAGTAAGAACACAGAGCGGCTTTTACAGGCAAGAGAGAA 410
1081 CTCAGAGAGCTCTGTATCTGTAGCGAAGCAAGCGGCAAGCGGCGAGGCTGCTCAAG 1140
DB CTCAGAGAGCTCTGTATCTGTAGCGAAGCAAGCGGCAAGCGGCGAGGCTGCTCAAG 470
411 CTCAGAGAGCTCTGTATCTGTAGCGAAGCAAGCGGCGAGGCTGCTCAAG 470
1141 CGCCATGACTGGGAGGGGATGCTGCTCTTCCCAATATGCCAGAGAGAGATGATAG 1200
DB CGCCATGACTGGGAGGGGATGCTGCTCTTCCCAATATGCCAGAGAGAGATGATAG 530
471 CGCCATGACTGGGAGGGGATGCTGCTCTTCCCAATATGCCAGAGAGAGATGATAG 530
1201 GTAGCTTGTGTAGCGCTCGAAGAAATGAGACGGGCTGGGCTTTGTTGTGCTGCA 1260
DB GTAGCTTGTGTAGCGCTCGAAGAAATGAGACGGGCTGGGCTTTGTTGTGCTGCA 590
531 GTAGCTTGTGTAGCGCTCGAAGAAATGAGACGGGCTGGGCTTTGTTGTGCTGCA 590
1261 CTGAACCTCTCTCTATCTTGACATCTCCGGTGTGTTTGTACATATAATTAATTG 1320
DB CTGAACCTCTCTCTATCTTGACATCTCCGGTGTGTTTGTACATATAATTAATTG 648
591 CTGAACCTCTCTCTATCTTGACATCTCCGGTGTGTTTGTACATATAATTAATTG 648
1321 CCGGTGGCTCAACGTAAAT 1342
DB CCGGTGGCTCAACGTAAAT 670
649 CCGGTGGCTCAACGTAAAT 670
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RESULT 9
LOCUS BU270799 414 bp mRNA linear EST 09-APR-2002
DEFINITION BU270799 Y. Ogihara unpublished cDNA library, wh_ch Triticum
aestivum cDNA clone wh09sk12 5', mRNA sequence.
ACCESSION BU270799
VERSION BU270799.1 GI:20096467
KEYWORDS EST
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 414)
AUTHORS Ogihara, Y. and Murai, K.
TITLE Expressed genes in Triticum aestivum
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..414
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="wh09sk12"
/tissue_type="pistil at heading date"
/dev_stage="Feekes' scale 10.5"
/clone_lib="Y. Ogihara unpublished cDNA library, wh_ch"
ORIGIN
Query Match 26.7%; Score 358.4; DB 12; Length 414;
Best Local Similarity 97.9%; Pred. No. 3.2e-94;
Matches 374; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
QY 961 GAACATCCGATGACACAGGCGCGCTCTTCTCGGTGACACTCCGAGCAAGTCCG 1020
DB 3 GAACATCCGATGACACAGGCGCGCTCTTCTCGGTGACACTCCGAGCAAGTCCG 62
QY 1021 GTGCTGTATGCCCTTACAGAGTAAGAACCAAGCAGCGCTTTTACAGAGGCAAGAGAGA 1080
DB 63 GTGCTGTATGCCCTTACAGAGTAAGAACCAAGCAGCGCTTTTACAGAGGCAAGAGAGA 122
QY 1081 CTCACAGAGACTGTGATGCTGAGCGAAGGAGGAGGAGCGGCGAGGCTGCTCCAA 1140
DB 123 CTCACAGAGACTGTGATGCTGAGCGAAGGAGGAGGAGGAGCGGCGAGGCTGCTCCAA 182
QY 1141 CGGCATGACTGGAGGAGGAGTGTGCTCTTCCAGATGCCAGAGAGAGAGATGATAG 1200
DB 183 CGGCATGACTGGAGGAGGAGTGTGCTCTTCCAGATGCCAGAGAGAGAGATGATAG 242
QY 1201 GTAGCTTGTGTGAGCGCTGAAAGAAATGACGGGCTGGGCTGTTGTGTGTCTGCA 1260
DB 243 GTAGCTTGTGTGAGCGCTGAAAGAAATGACGGGCTGGGCTGTTGTGTGTCTGCA 302
QY 1261 CTGAACCTCTCTCTATCTTGCATCTCCGGTGTGTTTGTATCATATTAATATTG 1320
DB 303 CT-ACCCTCTCTATCTTGCATCTCCGGTGTGTTTGTATCATATTAATATTG 360
QY 1321 CCCGTGCGCTCAACGTGAAT 1342
DB 361 CCCGTGCGCTCAACGTGAAT 382
RESULT 10
LOCUS BU232268 491 bp mRNA linear EST 05-APR-2002
DEFINITION BU232268 Y. Ogihara unpublished cDNA library, wh_e Triticum

ACCESSION BU232268
VERSION BU232268.1 GI:20050073
KEYWORDS EST
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 491)
AUTHORS Ogihara, Y. and Murai, K.
TITLE Expressed genes in Triticum aestivum
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..491
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whelm24"
/tissue_type="seed DPA10"
/dev_stage="Feekes' scale 11.2"
/clone_lib="Y. Ogihara unpublished cDNA library, wh_e"
ORIGIN
Query Match 26.7%; Score 358.4; DB 12; Length 491;
Best Local Similarity 97.9%; Pred. No. 3.4e-94;
Matches 374; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
QY 961 GAACATCCGATGACACAGGCGCGCTCTTCTCGGTGACACTCCGAGCAAGTCCG 1020
DB 88 GAACATCCGATGACACAGGCGCGCTCTTCTCGGTGACACTCCGAGCAAGTCCG 147
QY 1021 GTGCTGTATGCCCTTACAGAGTAAGAACCAAGCAGCGCTTTTACAGAGGCAAGAGAGA 1080
DB 148 GTGCTGTATGCCCTTACAGAGTAAGAACCAAGCAGCGCTTTTACAGAGGCAAGAGAGA 207
QY 1081 CTCACAGAGACTGTGATGCTGAGCGAAGGAGGAGGAGCGGCGAGGCTGCTCCAA 1140
DB 208 CTCACAGAGACTGTGATGCTGAGCGAAGGAGGAGGAGGAGCGGCGAGGCTGCTCCAA 267
QY 1141 CGGCATGACTGGAGGAGGAGTGTGCTCTTCCAGATGCCAGAGAGAGAGATGATAG 1200
DB 268 CGGCATGACTGGAGGAGGAGTGTGCTCTTCCAGATGCCAGAGAGAGAGATGATAG 327
QY 1201 GTAGCTTGTGTGAGCGCTGAAAGAAATGACGGGCTGGGCTGTTGTGTGTCTGCA 1260
DB 328 GTAGCTTGTGTGAGCGCTGAAAGAAATGACGGGCTGGGCTGTTGTGTGTCTGCA 387
QY 1261 CTGAACCTCTCTCTATCTTGCATCTCCGGTGTGTTTGTATCATATTAATATTG 1320
DB 388 CT-ACCCTCTCTATCTTGCATCTCCGGTGTGTTTGTATCATATTAATATTG 445
QY 1321 CCCGTGCGCTCAACGTGAAT 1342
DB 446 CCCGTGCGCTCAACGTGAAT 467
RESULT 11
LOCUS CK153053 897 bp mRNA linear EST 05-DEC-2003
DEFINITION FGAS031606 Triticum aestivum FGAS: Talc2 Triticum aestivum cDNA,
mRNA sequence.
ACCESSION CK153053
VERSION CK153053.1 GI:38972724
KEYWORDS EST.

Source	Organism	Reference Authors	Title Journal Comment
	Triticum aestivum (bread wheat)		
	Triticum aestivum		
	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.		
	1 (bases 1 to 897)		
	Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Larchoe, A., Pennel, C., Roach, J.L. and Searns, F.		
	Functional Genomes of Abiotic Stress In Wheat and Canola Crops Unpublished (2003)		
	Contact: Wm L Crosby		
	Bioinformatics		
	University of Saskatchewan, Department of Computer Science		
	1C101 Engineering Building, 57 Campus Drive, Saskatoon,		
	Saskatchewan, S7N 5A9, Canada		
	Tel: 306 966 1769		
	Fax: 306 966 2033		
	Email: fgas.ests@cs.usask.ca		
	This sequence is the direct result of the Base calling software		
	phred (default parameters). It is the raw base calls. To aid in the		
	identification of the high quality insert the software Lucy		
	(default parameters) has been run on this sequence. Lucy identified		
	the region 125,627.		
	Plate: Talc237 row: A column: 20.		
	Location/Qualifiers		
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	/cultivar="wheat line CT 14106"		
	/db_xref="taxon:4565"		
	/lab_host="DH5 alpha"		
	/clone_lib="Triticum aestivum FGAS; Talc2"		
	/note="Organ: Crown; Vector: pGEM-T; SSH (suppression		
	subtractive hybridization) cDNA library from genotype		
	CI14106 cold hardened at 2 C for 1 day (24 h) (tester) and		
	subtracted against genotype Norstar cold hardened at 2 C		
	for 21 days and 49 days (equal amount of cDNA pooled		
	together before subtraction, driver). Nitro-pyole		
	anchored oligo-dt priming and non-directional cloning."		
Query Match	26.7%; Score 358.4; DB 14; Length 897;		
Best Local Similarity	97.9%; Pred. No. 4.3e-94;		
Matches 374; Conservative	0; Mismatches 6; Indels 2; Gaps 1;		
961	GAACATCCGATGACACAGGCGCGCTCTTCGCGGTACATCCGAGCAACTGCG	10220	
540	GAACATCCGATGACACAGGCGCGCTCTTCGCGGTACATCCGAGCAACTGCG	481	
1021	GTCGTGATGCCCTTACAGAGTAAGAACACAGCGCGCTTGTACAGCAAGAGAGA	10860	
480	GTCGTGATGCCCTTACAGAGTAAGAACACAGCGCGCTTGTACAGCAAGAGAGA	421	
1081	CTCCAGAGAGTGTGTGATCGTGAAGCAAGGAGGAGGCGCGAGCTGCTCCAG	11480	
420	CTCCAGAGAGTGTGTGATCGTGAAGCAAGGAGGAGGCGCGAGCTGCTCCAG	361	
1141	CGCCATACCTGAGGAGGAGTGTGCTCTTCCCAAGATCCGAGAGAGAGATGATAG	12000	
360	CGCCATACCTGAGGAGGAGTGTGCTCTTCCCAAGATCCGAGAGAGAGATGATAG	301	
1201	GTAAGCTGTGTGTGAGCGCTGAAAGAAATGACGCGCTGTGTGTGTGTGTGCTGA	12600	
300	GTAAGCTGTGTGTGAGCGCTGAAAGAAATGACGCGCTGTGTGTGTGTGTGCTGA	241	
1261	CTGAACCTCTCTCTATCTTGCACATTCGCGGATGTTTGTATCATATTAATTAATG	13200	
240	CT--ACCTCTCTCTATCTTGCACATTCGCGGATGTTTGTATCATATTAATTAATG	183	
1321	CCGCTGCGCTCAACGTGAAT 1342		

RESULT 12				
LOCUS	Bt273375/c	721 bp	mRNA	linear EST 09-Apr-2002
DEFINITION	Bt273375 Y. Ogihara unpublished cDNA library, Wh_ch Triticum aestivum cDNA clone whol16p06 3', mRNA sequence.			
ACCESSION	Bt273375			
VERSION	Bt273375.1	GI:20098160		
KEYWORDS	EST,			
SOURCE	Triticum aestivum (bread wheat)			
ORGANISM	Triticum aestivum			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.			
AUTHORS	Ogihara,Y. and Murai,K.			
TITLE	Expressed genes in Triticum aestivum			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yatae, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tahin@genes.nig.ac.jp. Location/Qualifiers			
FEATURES				
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ORIGIN				
Query Match	26.3%; Score 353.8; DB 12; Length 721;			
Best Local Similarity	97.4%; Pred. No. 9e+93;			
Matches 370; Conservative	0; Mismatches 8; Indels 2; Gaps 1;			
Dy	961 GAACATCCGATGACAACAGCGCGCTCTTTCTCGGTGTAACCTCCGAGCAGACTGCG 1020			
Db	383 GAACATCCGATGACAACAGCGCGCTCTTTCTCGGTGTAACCTCCGAGCAGAACTGCG 324			
Dy	1021 GTGGTGATGCCCTTAGAGATGAAGCAAGCGCGCTTTTACAGAGCAAAGAGAA 1080			
Db	323 GTGGTGATGCCCTTAGAGATGAAGCAAGCGCGCTTTTACAGAGCAAAGAGAA 264			
Dy	1081 CTCAGAGAGTCGTGATCGTGAGCGAAGCGAGCGCAACGGCGCGAGCGTGCTCCAG 1140			
Db	263 CTCAGAGAGTCGTGATCGTGAGCGAAGCGAGCGCAACGGCGCGAGCGTGCTTAAG 204			
Dy	1141 CGCATATCTGAGAGGGGATCGGCCCTTCCCAGATGCAGAGAGAGAGATGAGTAG 1200			
Db	203 CGCATATCTGAGAGGGGATCGGCCCTTCCCAGATGCAGAGAGAGAGATGAGTAG 144			
Dy	1201 GTAAGTTGTTGTTAGAGGCTCGAAAAGAAATGACGCGGCTGGTGTGTTGTGCTGCA 1260			
Db	143 GTAAGTTGTTGTTAGAGGCTCGAAAAGAAATGACGCGGCTGGTGTGTTGTGCTGCA 84			
Dy	1261 CTGAACCTCTCTCTATCTTGACATTCCTCCGATTGTTTTGTATATATAATAATTG 1320			
Db	83 CT--ACCCTCTCTATATCTTGACATTCCTCCGATTGTTTTGTATATATAATAATTG 26			
Dy	1321 CCGGTGCGCTCAAGGTGAA 1340			
Db	25 CCGGTGCGCTCAACANAACA 6			

CD934119
 LOCUS CD934119 527 bp mRNA EST 15-JUL-2003
 DEFINITION GR45.123424F010723 GR45 Triticum aestivum cDNA clone GR45123A24,
 mRNA sequence.
 ACCESSION CD934119
 VERSION CD934119.1 GI:32781883
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 REFERENCE 1 (bases 1 to 527)
 AUTHORS Genopiante.
 TITLE Genopiante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genopiante
 Genopiante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genopiante' (<http://www.genopiante.com>
 and <http://genopiante-info.infobiogen.fr>).
 Location/Qualifiers
 1..527
 /organism="Triticum aestivum"
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 /culivar="rectal"
 /db_xref="taxon:4565"
 /clone="GR45123A24"
 /tissue_type="grain (45 degrees per day after
 pollination)"
 /clone_1ib="GR45"

ORIGIN

Query Match 25.9%; Score 347.6; DB 14; Length 527;
 Best Local Similarity 96.2%; Pred. No. 5.4e-91;
 Matches 356; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 961 GAATATCCGATGACAGAGCCCGCTCTTCTGCGTACACCTCCGACGAAGTGG 1020
 DB 135 GAATATCCGATGACAGAGCCCGCTCTTCTGCGTACACCTCCGACGAAGTGG 194
 QY 1021 GTCTGTATGCCCTTACAGAGTAAGAACGACGAGCGCTTTGTTACAAGCAAGAGAA 1080
 DB 195 GTCTGTATGCCCTTACAGAGTAAGAACGACGAGCGCTTTGTTACAAGCAAGAGAA 254
 QY 1081 CTCACAGAGCTGTGATGCTGAGCGAAGCGAGCGGCAACGCGCGAGCTGCTCAAG 1140
 DB 255 CTCACAGAGCTGTGATGCTGAGCGAAGCGAGCGGCAACGCGCGAGCTGCTCAAG 314
 QY 1141 CGCATGACTGGAGAGGGAGTGTGCTCTTCCCAAGTGCACGAGGACAGATGATAG 1200
 DB 315 CGCATGACTGGAGAGGGAGTGTGCTCTTCCCAAGTGCACGAGGACAGATGATAG 374
 QY 1201 GTAGCTTGTGTGAGACCGCTCGAAGAAATGAGACGGGCTGGGTGTTGTGCTGCA 1260
 DB 375 GTAGCTTGTGTGAGACCGCTCGAAGAAATGAGACGGGCTGGGTGTTGTGCTGCA 434
 QY 1261 CTGAACCTCTCTCTATCTTGCACATTCGCGGTTGTTTGTACATATAATAATTG 1320
 DB 435 CTGAACCTCTCTCTATCTTGCACATTCGCGGTTGTTTGTACATATAATAATTG 494
 QY 1321 CCGGTGGGCT 1330
 DB 495 CCGGTGGGCT 504

RESULT 14
 LOCUS CD899313 532 bp mRNA linear EST 14-JUL-2003
 DEFINITION G174.11021F010825 G174 Triticum aestivum cDNA clone G17411021,

CD899313
 LOCUS CD899313 532 bp mRNA linear EST 14-JUL-2003
 DEFINITION G174.105D15F010823 G174 Triticum aestivum cDNA clone G174105D15,
 mRNA sequence.
 ACCESSION CD897227
 VERSION CD897227.1 GI:32671555
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 REFERENCE 1 (bases 1 to 532)
 AUTHORS Genopiante.
 TITLE Genopiante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genopiante
 Genopiante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genopiante' (<http://www.genopiante.com>
 and <http://genopiante-info.infobiogen.fr>).
 Location/Qualifiers
 1..532
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /culivar="rectal"
 /db_xref="taxon:4565"
 /clone="G17411021"
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 pollination)"
 /clone_1ib="G174"

ORIGIN

Query Match 25.9%; Score 347.6; DB 14; Length 532;
 Best Local Similarity 96.2%; Pred. No. 5.4e-91;
 Matches 356; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 961 GAATATCCGATGACAGAGCCCGCTCTTCTGCGTACACCTCCGACGAAGTGG 1020
 DB 135 GAATATCCGATGACAGAGCCCGCTCTTCTGCGTACACCTCCGACGAAGTGG 194
 QY 1021 GTCTGTATGCCCTTACAGAGTAAGAACGACGAGCGCTTTGTTACAAGCAAGAGAA 1080
 DB 195 GTCTGTATGCCCTTACAGAGTAAGAACGACGAGCGCTTTGTTACAAGCAAGAGAA 254
 QY 1081 CTCACAGAGCTGTGATGCTGAGCGAAGCGAGCGGCAACGCGCGAGCTGCTCAAG 1140
 DB 255 CTCACAGAGCTGTGATGCTGAGCGAAGCGAGCGGCAACGCGCGAGCTGCTCAAG 314
 QY 1141 CGCATGACTGGAGAGGGAGTGTGCTCTTCCCAAGTGCACGAGGACAGATGATAG 1200
 DB 315 CGCATGACTGGAGAGGGAGTGTGCTCTTCCCAAGTGCACGAGGACAGATGATAG 374
 QY 1201 GTAGCTTGTGTGAGACCGCTCGAAGAAATGAGACGGGCTGGGTGTTGTGCTGCA 1260
 DB 375 GTAGCTTGTGTGAGACCGCTCGAAGAAATGAGACGGGCTGGGTGTTGTGCTGCA 434
 QY 1261 CTGAACCTCTCTCTATCTTGCACATTCGCGGTTGTTTGTACATATAATAATTG 1320
 DB 435 CTGAACCTCTCTCTATCTTGCACATTCGCGGTTGTTTGTACATATAATAATTG 494
 QY 1321 CCGGTGGGCT 1330
 DB 495 CCGGTGGGCT 504

RESULT 15
 LOCUS CD897227 565 bp mRNA linear EST 14-JUL-2003
 DEFINITION G174.105D15F010823 G174 Triticum aestivum cDNA clone G174105D15,
 mRNA sequence.
 ACCESSION CD897227
 VERSION CD897227.1 GI:32671555

KEYWORDS

EST.
Triticum aestivum (bread wheat)

SOURCE

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticaceae; Triticum.

1 (bases 1 to 565)

Genoplane, a major partnership french program in plant genomics

Unpublished (2003)

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This sequence has been generated in the framework of the french

plant genomics programme 'Genoplane' (<http://www.genoplane.com>and <http://genoplane-info.infobiogen.fr>).

Location/Qualifiers

1..565

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/db_xref="taxon:4565"

/clone="G174105D15"

/tissue_type="grain (174 degrees per day after

pollination)"

/clone_idb="G174"

ORIGIN

Query Match 25 9%; Score 347.6; DB 14; Length 565;

Best Local Similarity 96.2%; Pred.No.5.6e-91;

Matches 356; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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DB 170 GAACATCGCATGACATAGCGCGCTCTTCTGTACACTCTAGCAACTGCG 229

QY 1021 GTCGTATGCGCTTACAGAGTAAGACAGCGCGCTTGTACAGGCAAGAGAGAA 1080

DB 230 GTCGTATGCGCTTACAGAGTAAGACAGCGCGCTTGTACAGGCAAGAGAGAA 289

QY 1081 CTCCAGAGAGCTCGTGAATCGAGCAAGCAAGCGGCAACGCGGAGCTGCTCCAAG 1140

DB 290 CTCCAGAGAGCTCGTGAATCGAGCAAGCAAGCGGCAACGCGGAGCTGCTCCAAG 349

QY 1141 CGCCATGACTGGAGGAGATCGTGCCTCTTCCCAAGATGCCAGAGAGAGATGATAG 1200

DB 350 CGCCATGACTGGAGGAGATCGTGCCTCTTCCCAAGATGCCAGAGAGATGATAG 409

QY 1201 GTAGCTTGTGGTGAAGCGGCTGCAAGAAATGACGCGGCTGGGTGTTGTGTGCTGCA 1260

DB 410 GTAGCTTGTGGTGAAGCGGCTGCAAGAAATGACGCGGCTGGGTGTTGTGTGCTGCA 469

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DB 530 CCGGTGCGCT 539

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